

[illegible]

1692 CCGGAGAGGCTTACCATGAAATCCAAAGCCATCCGAGGACTAGAGGCCAGCGGAT 1751
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1752 GCTCTGAGTGGCAAGCGGAGAGTACAGTACAGGAGCTCTGCGCCCTGATACGGCTCAA 1811
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1812 CTTCTGAGAGCTGACAGTACAGGAGGAGTACAGGAGTACAGGAGTACAGGAGTACAG 1871
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1872 TCTGTTGAGAGCTGACAGTACAGGAGGAGTACAGGAGTACAGGAGTACAGGAGTACAG 1931
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DB 2264 CTACTCCCGTCACAGCCGCAAGCCCTACCTGCAAGGCTTACGAGGGTGCCTCTCTCT 2323
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DB 2924 AGTSCAAGACCTGGGCAAGCACTGACAAAGTACTGCTACAAAGAACTGCTGCTGCAAGCC 2983
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DB 2984 CCGTGAAGCCCTTGGGCTCAGCGCAAGCTGACAAAGTACTGCTGCTGCAAGCGGAGGCACTC 3043
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DB 3044 GCTTGGAGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3103
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 4844 AACGGGCTGAGCT 4857

RESULT 4
 US-09-982-610-17/c
 Sequence 17, Application US/09982610
 Patent No. US2002014420A1
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 Goedel, David
 Bennett, Brian D.
 Lee, James M.
 Matthews, William
 Tsai, Siao Ping
 Wood, William I.
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE ANONIST ANTIBODIES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minitab (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/982,610
 FILING DATE: 17-Oct-2001
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/446,646
 FILING DATE: 1996-May-23
 APPLICATION NUMBER: 08/222616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P08218PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6827 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-982-610-17

Query Match 25.3% Score 1040.2; DB 10; Length 6827;
 Best Local Similarity 98.3%; Pred.No 7.1e-252;
 Matches 1051; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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RESULT 7

US-09-872-136-5

Sequence 5, Application US/09872136

Patent No. US2002019545A1

GENERAL INFORMATION:

APPLICANT: Lemischka, Thor R.

TITLE OF INVENTION: TGF- β 1-INDUCED HEMATOPOIETIC STEM CELL

Db 2845 AAGAGCTACGTCGAGCAATCCCTGTCATCTCGAAGCGCCCTGGACAGCATCCACCT 2904

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Qy 3311 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3370

Db 3265 TGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3324

Qy 3371 GTGACATCAATGAGAGCTTCTGCGACGCTGAGAGAGGAGAGAGAGAGAGAGAGAG 3430

Db 3325 GTAAAGATGATGAGAGATTTTGTAGCGATTTGAAGAGAGATGAGAGAGAGAGAG 3384

Qy 3431 GAGCTGCGCATCTGCGCATAGCGGCTATCTGAGATCTGCTGCTGCTGCTGCTGCTG 3490

Db 3385 GATATCTTAACCGAAGATGAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3444

Qy 3491 GCGAGAGCTGCAATCTGCGAGCTGTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 3550

Db 3445 CAGAGAGCGAGCTTTCAGAGTTGTGAGAGATTTGAGAGATTTGAGAGATTTGAGAG 3504

Qy 3551 CTGGAAG 3567

Db 3505 CAGCAGAGATGCGCAAGA 3521

RESULT 10

US-09-970-088-9

Sequence 9, Application US/09970088

Patent No. US20020151489A1

GENERAL INFORMATION:

APPLICANT: GRAVEREAUX, EDWIN C.

APPLICANT: SILVER, MARCY

APPLICANT: ISNER, JEFFREY M.

APPLICANT: YOON, YOUNG-SUP

TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC

FILE REFERENCE: 71417/55062

CURRENT APPLICATION NUMBER: US/09/970,088

PRIOR APPLICATION NUMBER: 2001-10-02

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 9

LENGTH: 420

TYPE: DNA

ORGANISM: Homo sapiens

US-09-970-088-9

Query Match 10.2% Score 420; DB 10; Length 420;

Host Local Similarity 100.0%; Pred. No. 4e-96;

Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2111 CAGGCTTGTCGCGGAGAGCGGACCGCCCGAGATGCTGTGTACAAAGACGAGAGCTG 2170

Db 1 CAGGCTTGTCGCGGAGAGCGGACCGCCCGAGATGCTGTGTACAAAGACGAGAGCTG 60

Qy 2171 CTGAGAGAAAGTCTGAGAGTCTGAGTCTGCGAGATCCCAAGAGAGTGTGACATCCAGGCG 2230

Db 61 CTGAGAGAAAGTCTGAGAGTCTGAGTCTGCGAGATCCCAAGAGAGTGTGACATCCAGGCG 120

Qy 2231 GTGCGGAGAGAGATGCGGAGAGCTATCTGTGAGGCTGTGCAAGCGGCTGCTG 2290

Db 121 GTGCGGAGAGAGATGCGGAGAGCTATCTGTGAGGCTGTGCAAGCGGCTGCTG 180

Qy 2291 AACTCTCCCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2350

Db 181 AACTCTCCCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

Qy 2351 ATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2410

Db 241 ATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

Qy 2411 TGTACATGAGAGAGCGCGCCACGAGACATCAAGAGGAGCTACCTGTCCATCATG 2470

Db 301 TGTACATGAGAGAGCGCGCCACGAGACATCAAGAGGAGCTACCTGTCCATCATG 360

Qy 2471 GACCGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2530

Db 361 GACCGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

RESULT 11

US-09-970-088-7

Sequence 7, Application US/09970088

Patent No. US20020151489A1

GENERAL INFORMATION:

APPLICANT: GRAVEREAUX, EDWIN C.

APPLICANT: SILVER, MARCY

APPLICANT: ISNER, JEFFREY M.

APPLICANT: YOON, YOUNG-SUP

TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC

FILE REFERENCE: 71417/55062

CURRENT APPLICATION NUMBER: US/09/970,088

PRIOR APPLICATION NUMBER: 2001-10-02

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 420

TYPE: DNA

ORGANISM: Oryctolagus cuniculus

US-09-970-088-7

Query Match 8.7% Score 356; DB 10; Length 420;

Best Local Similarity 90.5%; Pred. No. 4.9e-80;

Matches 380; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 2111 CAGTCTGTGTCGCGGAGAGCGGCGCCAGCATGCTGTGTACAAAGAGAGAGCTG 2170

Db 1 CAGTCTGTGTCGCGGAGAGCGGCGGAGAGCGGCGCCAGCATGCTGTGTACAAAGAGAGAGCTG 60

Qy 2171 CTGAGAGAAAGTCTGAGAGTCTGAGTCTGCGAGATCCCAAGAGAGTGTGACATCCAGGCG 2230

Db 61 CTGAGAGAAAGTCTGAGAGTCTGAGTCTGCGAGATCCCAAGAGAGTGTGACATCCAGGCG 120

Qy 2231 GTGCGGAGAGAGATGCGGAGAGCTATCTGTGAGGCTGTGCAAGCGGCTGCTG 2290

Db 121 GTGCGGAGAGAGATGCGGAGAGCTATCTGTGAGGCTGTGCAAGCGGCTGCTG 180

Qy 2291 AACTCTCCCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2350

Db 181 AACTCTCCCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY	2529	AGTGGAAATCCCGCCGACAGAGAGCTGACCTGGGAGAGAGTCCCGGCTAGAGGGGGCTTCG	2589
Db	2021	AGTGGAGATCCCGCCGACAGAGAGCTGACCTGGGAGAGAGTCCCGGCTAGAGGGGGCTTCG	2080
QY	2589	GGAGAGTGGTGGAAAGCTTCGACTTGGGATCCAGAGGGGACAGAGCTGACAGCCGTGG	2648
Db	2081	GGAGAGTGGTGGAAAGCTTCGACTTGGGATCCAGAGGGGACAGAGCTGACAGCCGTGG	2140
QY	2649	CCGTGAAAATGCTGAAAAGAGGGGCGCCACGCGCAGCGAGCAACGCGCGCTGATGTGGAGC	2708
Db	2141	CGTGAAGATGCTGAAAAGAGGGGCGCCACGCGCAGCGAGCAACGCGCGCTGATGTGGAGC	2200
QY	2709	TGAAGATCCTATTACATTCGCGCAGCAGCAGCTGAGCTGGTACAGCCCTGCTCGGGGGGTGCA	2768
Db	2201	TGAAGATCCTATTACATTCGCGCAGCAGCAGCTGAGCTGGTACAGCCCTGCTCGGGGGGTGCA	2260
QY	2769	CCAAAGCCGAGAGGCGCGCTCATGGGTATGGTGGAGTTCTGCAAGTAGAGGCAACCTCTCCA	2828
Db	2261	CCAAAGCCGAGAGGCGCGCTCATGGGTATGGTGGAGTTCTGCAAGTAGAGGCAACCTCTCCA	2317
QY	2829	ATTCTCTGTCGCGCAAGCGGAGACCTTCAAGCTCTTCCGCGAGAGTCTCCGACAGC	2888
Db	2318	ATTCTCTGTCGCGCAAGCGGAGACCTTCAAGCTCTTCCGCGAGAGTCTCCGACAGC	2377
QY	2889	CGGAGAGCTCCGCGCGCATGGTGGAGCTGCGACGCTGATGAGAGAGCGCGCGGAGAGA	2948
Db	2378	CGGAGAGAGCTCCGCGCGCATGGTGGAGCTGCGACGCTGATGAGAGAGCGCGCGGAGAGA	2437
QY	2949	GGAGCAGAGGCTGCTCTTGCGAGAGCTCTCGAGACAGCGAGAGCGAGCGAGCGCTTTC	3008
Db	2438	GGAGCAGAGGCTGCTCTTGCGAGAGCTCTCGAGACAGCGAGAGCGAGCGAGCGCTTTC	2497
QY	3009	CA-----GACCAAGAGAGCTGAGAGCTGTGGCTGAGAGCGCGCTACACATGG	3053
Db	2498	CAAAATGATCTCTTCTGTAGAGAGAGCTGGATAGAGAGATGGAGAGCGCGCTCGAGACTTC	2557
QY	3054	AAGATCTGTCTCTACAGCTGTGAGAGTGGCGCAGAGAGAGAGTCTCGGCTCCGGA	3113
Db	2558	GGAGAGCTGCTCTACAGCTGTGAGAGTGGCGCAGAGAGAGAGTCTCGGCTCCGGA	2617
QY	3114	ATGAGTATGACAGATACCTGAGTATGCTGCAATATGCTGTGTGTGGAGAAAGAGAGTGGTA	3173
Db	2618	ATGAGTATGACAGATACCTGAGTATGCTGCAATATGCTGTGTGTGGAGAAAGAGAGTGGTA	2677
QY	3174	AGATCTTACCTTGGCTTGTGCGCGGGAATGTAAAGAGCCTACCTACCTGCGCAAG	3233
Db	2678	AGATCTTACCTTGGCTTGTGCGCGGGAATGTAAAGAGCCTACCTACCTGCGCAAG	2737
QY	3234	CGAGAGCTGCGCTGCGCTGAGAGTGAAGAGAGCGCGGAGAGAGAGTGTGCAAGAGGTACA	3293
Db	2738	CGAGAGCTGCGCTGCGCTGAGAGTGAAGAGAGCGCGGAGAGAGAGTGTGCAAGAGGTACA	2797
QY	3294	CGAGAGAGAGTACAGTGTGGTCTTGGAGTGGCTTCTGAGAGATCTTCTGCTGGGG	3353
Db	2798	CGAGTGAAGAGAGTGTGGTCTTGGAGTGGCTTCTGAGAGATCTTCTGCTGGGG	2857
QY	3354	CCCTCCGATACCTTGGGTTGAGATATATGAGAGATTCTGCGAGAGGCTGAGAGAGCGCA	3413
Db	2858	TGAATCCCTACAGCTTGGATCTGTGTGAGAGAGAGTCTATTAAGTGGTCAAGAGATGAT	2917
QY	3414	CAAGCAGAGAGGCGCGCGAGAGCTGGCAGCAGCTGGCAATAGCGCAATCATGATTAAGTGT	3473
Db	2918	ACCAATATGCGAGCTCATTTGGCGCGCAAGAAATATATACGATCATGAGAGCTGT	2977

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NAME/KEY: mat_peptide
LOCATION: 112-3006
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FEATURE:
NAME/KEY: sig_peptide
LOCATION: 31..111
NAME/KEY: CDS
LOCATION: 31..3069
SEQUENCE DESCRIPTION: SEQ ID NO: 1
us-09-919-408-1

Query Match 5.98; Score 242.8; DB 10; Length 3453;
Best Local Similarity 54.3%; Pred. No. 2.1e-51;
Matches 558; Conservative 0; Mismatches 437; Indels 33; Gaps 2;

QY 2520 ATGCCAGGCACTGAAATTCCTCCGAGACGCTGCTGCGGAGACGCTGCGGCTACG 2579
DB 1829 ATGACCTTAAGTGGAGCTTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 1888
QY 2580 GAGCTTGGGAAAGTCTGGAGAGCTTCCTCCGAGGAAATTAAGATTGGAGAGCTG 2639
DB 1889 GCGCTTGGGAAAGTCTGGAGAGCTTCCTCCGAGGAAATTAAGATTGGAGAGCTG 1948
QY 2640 ACGAGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2699
DB 1949 TCGAGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2008
QY 2700 TGTGAGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2759
DB 2009 TGTGAGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2068
QY 2760 GGGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2819
DB 2069 GGGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2128
QY 2820 ACGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2879
DB 2129 TGTGAGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2188
QY 2880 GCGAGCA-----GGCGAGCTTCCGGCTGCTG 2911
DB 2189 ACGAGCAATTAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2248
QY 2912 GAGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2971
DB 2249 GTTCAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2308
QY 2972 TTCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 3025
DB 2309 CAATTCAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2368
QY 3027 ACGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 3086
DB 2369 ACGAGATTTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2428
QY 3087 GAGGATTTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 3146
DB 2429 AAGGATTTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2488
QY 3147 TTCTGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 3206
DB 2489 TGTGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2548
QY 3207 ACGAGATTTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 3266
DB 2549 TCGAGATTTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2608
QY 3267 CTGAAGATTTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 3326
DB 2609 CCGAGATTTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2668
QY 3327 TTCTGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 3386
DB 2669 TTCTGCTGAGGAAATTCCTCCGAGGAAATTAAGATTGGAGAGCTGCGGCTG 2728

QY 3387 ACTTCGCGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3446
DB 2729 ACTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2788
QY 3447 CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3506
DB 2789 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2848
QY 3507 CCGAGGCTG 3514
DB 2849 CCGAGGCTG 2856

Search completed: May 1, 2003, 14:17:14
Job time: 495 secs

QY	1081	GCCTGTAAAGCTGTGCAAGCTACCCCCCGCCCAAGTTCACAGTGTACAAAGATCGAAAGGC	1140
Db	1081	GCCCCGTAAAGCTGTGCAAGGTAACCCCCCGCCCAAGTTCACAGTGTACAAAGATCGAAAGGC	1140
QY	1141	ACTTCGGGGGCGCCACAGTGCACATGCCCTGGTGGCCAAAGAGGTGCACAGGCCTCAGAC	1200
Db	1141	ACTTCGGGGGCGCCACAGTGCACATGCCCTGGTGGCTCAAGAGGTGCACAGGCCTCAGAC	1200
QY	1201	AGGCACTACACCCCTGGCCCTGTGGAACTCCCGTGTGGCTGAGAGCGCAATCAGCCT	1260
Db	1201	AGGCACTACACCCCTGGCCCTGTGGAACTCCCGTGTGGCTGAGAGCGCAATCAGCCT	1260
QY	1261	GGAGCTGTGTGTGAATGTGGCCCGCCCGAGATACATGAGAAAGAGGCCTCTCCCGCAGAT	1320
Db	1261	GGAGCTGTGTGTGAATGTGGCCCGCCCGAGATACATGAGAAAGAGGCCTCTCCCGCAGAT	1320
QY	1321	CTACTCGCTCACAGCCGCCAGGCCCTCACTCTCAACAGGCTACAGGGTGGCCCTGCTCT	1380
Db	1321	CTACTCGCTCACAGCCGCCAGGCCCTCACTCTCAACAGGCTACAGGGTGGCCCTGCTCT	1380
QY	1381	CAGATCCAGTGTGGCACTGGGGGGCCCTGGAGAACCTGTGCAAGATGTTTGCCCAAGCTAGT	1440
Db	1381	CAGATCCAGTGTGGCACTGGGGGGCCCTGGAGAACCTGTGCAAGATGTTTGCCCAAGCTAGT	1440
QY	1441	CCGGCGCGCGGCAAGCAGCAAGACCTCATGCGCCACAGTCCCGTACAGCAAGAGGCGGTGACAC	1500
Db	1441	CCGGCGCGCGGCAAGCAGCAAGACCTCATGCGCCACAGTCCCGTACAGCAAGAGGCGGTGACAC	1500
QY	1501	GCAGGATGCCGTGAAACCCATCCAGAGACCTGGACACTTGGACCGAGTTTGTGAGAGAAA	1560
Db	1501	GCAGGATGCCGTGAAACCCATCCAGAGACCTGGACACTTGGACCGAGTTTGTGAGAGAAA	1560
QY	1561	GAATTAACACTGTGAGACAGCTGTGGATATCCAGAAATGCAAGAGTGTCCATGTACAAAGTG	1620
Db	1561	GAATTAACACTGTGAGACAGCTGTGGATATCCAGAAATGCAAGAGTGTGTCTGCAATGTACAAAGTG	1620
QY	1621	TGTGGTCTCCAAACAAGTGTGGCCAGAGTAGAGCGGCTCATCTACTTATGTGACCAAGAT	1680
Db	1621	TGTGGTCTCCAAACAAGTGTGGCCAGAGTAGAGCGGCTCATCTACTTATGTGACCAAGAT	1680
QY	1681	CCCCGAGGCTTCACCATCCGATCCGATCCGAAGGCAATCCGAGAGCATATAGAGGCCAAGCCGT	1740
Db	1681	CCCCGAGGCTTCACCATCCGATCCGATCCGAAGGCAATCCGAGAGCATATAGAGGCCAAGCCGT	1740
QY	1741	GCTCTGAGCTGCAAGGCGCAAGCACTACAAAGTACAGAGATGTGGCGTGTACCGGCTCAA	1800
Db	1741	GCTCTGAGCTGCAAGGCGCAAGCACTACAAAGTACAGAGATGTGGCGTGTACCGGCTCAA	1800
QY	1801	CTGTGCGACGCTGACAGATGTGGCAATGTGGCAATCCGAGTTTGTGTGACATGCAAGAAGTGTCA	1860
Db	1801	CTGTGCGACGCTGACAGATGTGGCAATGTGGCAATCCGAGTTTGTGTGACATGCAAGAAGTGTCA	1860
QY	1861	TCTGTGGCCACCCCTCTGGGCGGTCAAGCTGTGAGAGAGGTGTGCACCTGTGGCGCGCCAGC	1920
Db	1861	TCTGTGGCCACCCCTCTGGGCGGTCAAGCTGTGAGAGAGGTGTGCACCTGTGGCGCGCCAGC	1920
QY	1921	CACCGTCACCTGAGTATCCCGCGGTGCGCGCCAGCAGCAGAGGGCTACTATGTGTGGA	1980
Db	1921	CACCGTCACCTGAGTATCCCGCGGTGCGCGCCAGCAGCAGAGGGCTACTATGTGTGGA	1980
QY	1981	AGTGCAGAGCCGGGACACCATGACAAAGAGTGTGCACAAAGAGTACTGTGTGGTGCAGCG	2040
Db	1981	AGTGCAGAGCCGGGACACCATGACAAAGTGTGCACAAAGAGTACTGTGTGGTGCAGCG	2040
QY	2041	CTTGCAGAGCCCTCGGCTCAACGAGAACTTGACGCAACCTCTGGTGAACGTAGAGGACTC	2100
Db	2041	CTTGCAGAGCCCTCGGCTCAACGAGAACTTGACGCAACCTCTGGTGAACGTAGAGGACTC	2100
QY	2101	GCTGGAGAGTACAGTGTGTGTGGTGTGGCGGACGACGCGCCCGCCAGCATGTGTGTGTACAAAGA	2160
Db	2101	GCTGGAGAGTACAGTGTGTGTGGTGTGGCGGACGACGCGCCCGCCAGCATGTGTGTGTACAAAGA	2160
QY	2161	CGAGAGGCTGTGTGAGAGAGAAAAGTCTGAGATGTGACTTGGCGGACTCTCCACGAACTCTAG	2220

Db	3241	CGGCTGCGCCCTCAAGTGGATGCGCCCTGAAAGCATCTTCACAGAGTGTACACACAGCA	3360
Qy	3301	GAGTACAGCTGTGCTCTTTGGGATGCTTCTCTGGGAGATCTTCTCTGGAGGACCTCCCC	3360
Db	3301	GAGTACAGCTGTGCTCTTTGGGATGCTTCTCTGGGAGATCTTCTCTGGAGGACCTCCCC	3360
Qy	3361	GTACCGCTGGGGTCCAGATCATATAGAGAGTGTCTCCACGGGCTGAGAGAGCGCCAAAGAT	3420
Db	3361	GTACCGCTGGGGTCCAGATCATATAGAGAGTGTCTCCACGGGCTGAGAGAGCGCCAAAGAT	3420
Qy	3421	GAGGCGCCCGGAGCTGTGCCACATCCGACCCATACGACCGCATATCTGATCTGTGGG	3480
Db	3421	GAGGCGCCCGGAGCTGTGCCACATCCGACCCATACGACCGCATATCTGATCTGTGGG	3480
Qy	3541	GGGCGAGGCGCTCCCAAGAGCAAGAGAGAGGTTCGATGGCCCGCGCGAGCTGCAGAGTC	3600
Db	3541	GGGCGAGGCGCTCCCAAGAGCAAGAGAGAGGTTCGATGGCCCGCGCGAGCTGCAGAGTC	3600
Qy	3601	AGAAAGAGGTAGCTTCTCGCAGGTGTCCACACATGGCCCTACACATGCCCGAGCTCACGC	3660
Db	3601	AGAAAGAGGTAGCTTCTCGCAGGTGTCCACACATGGCCCTACACATGCCCGAGCTCACGC	3660
Qy	3661	TGAGGACACGCGCCGCCCAAGCTGTGAGGGCCACAGCTGTGGCGCGAGGTATACAACTGGT	3720
Db	3661	TGAGGACACGCGCGCCGCCCAAGCTGTGAGGGCCACAGCTGTGGCGCGAGGTATACAACTGGT	3720
Qy	3721	GTCTCTTCCGCGGATGCTGTGGCCAGAGGGGCTGAGACCGGTGGTCTCCAGCATGAAAGAC	3780
Db	3721	GTCTCTTCCGCGGATGCTGTGGCCAGAGGGGCTGAGACCGGTGGTCTCCAGCATGAAAGAC	3780
Qy	3781	ATTGAGGAATTTCCCATGACCCCTAACGACCTTACAAAGCTCTGTGGACAAACAGAGAGA	3840
Db	3781	ATTGAGGAATTTCCCATGACCCCTAACGACCTTACAAAGCTCTGTGGACAAACAGAGAGA	3840
Qy	3841	CAGTGGATGCTGCTGGCTGGAGAGAGGTTTACACAGTGAAGAGAGAGCATATACAGAGA	3900
Db	3841	CAGTGGATGCTGCTGGCTGGAGAGAGGTTTACAGAGAGTGAAGAGAGAGCATATACAGAGA	3900
Qy	3901	AAGCGGCTTACGCTGTAAAGAGACCTGTGCCAGATGTGGCTGTGACCAAGGACACACCTGA	3960
Db	3901	AAGCGGCTTACGCTGTAAAGAGACCTGTGCCAGATGTGGCTGTGACCAAGGACACACCTGA	3960
Qy	3961	CTCCCAAGAGAGCGCGCGCGCTGTAGAGGGGGGCTGAGAGGGCGACAGGTGTTTACAA	4020
Db	3961	CTCCCAAGAGAGCGCGCGCGCTGTAGAGGGGGGCTGAGAGGGCGCGAGGTGTTTACAA	4020
Qy	4021	CAGCGAGTATGAGGAGCTGTGGAGCCCAAGACGAGAGGACACTGTCTCCCGTGTGGCGG	4080
Db	4021	CAGCGAGTATGAGGAGCTGTGGAGCCCAAGACGAGAGGACACTGTCTCCCGTGTGGCGG	4080
Qy	4081	CGTGAATTCTTCACAGCAACACACTACTATA 4111	
Db	4081	CGTGAATTCTTCACAGCAACACACTACTATA 4111	
RESULT 2			
US-08-901-710-3			
: Sequence 3, Application us/08901710			
: Patent No. 6107046			
: GENERAL INFORMATION:			
: APPLICANT: Alltalo, Karl			
: APPLICANT: Appelkova, Olga			
: APPLICANT: Pajusola, Katri			
: APPLICANT: Armstrong, Elna			
: APPLICANT: Korhonen, Jaana			
: APPLICANT: Kaipainen, Arja			
: APPLICANT: Mälikäinen, Marja-Terttu			
: TITLE OF INVENTION: PT4, A RECEPTOR TYROSINE KINASE, AND USES			
: TITLE OF INVENTION: THEROOF			

RESULT 2
US-08-901-710-3
Sequence 3. Application US/08901710
Patent No. 6107046
GENERAL INFORMATION:
APPLICANT: Alltalo, Kari
APPLICANT: Aprelikova, Olga
APPLICANT: Pajusola, Katri
APPLICANT: Armstrong, Elina
APPLICANT: Korhonen, Jaana
APPLICANT: Kalpainen, Arja
APPLICANT: Mäkiläinen, Marja-Terttu
TITLE OF INVENTION: FIT4, A RECEPTOR TYROSINE KINASE, AND USES THEREOF


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Db 3601 AGAGAGGSSGAGCTTCTGCGAGGTGTCCAGCATTGSCCCTACACATGCCCCAGGCTGACCC 3660
QY 3661 TGAGGACAGCCCCCAAGCCCTGACGAGCCGACACACCTGGGCGCCAGGATTATCACTGGCT 3720
Db 3661 TGAGGACAGCCCCCAAGCCCTGACGAGCCGACACACCTGGGCGCCAGGATTATCACTGGCT 3720
QY 3721 GTCTTTCCCGGAGTCCCTGCGCAGAGGAGGCTGAGACCCGTTGCTTCCGAGATGAGAC 3780
Db 3721 GTCTTTCCCGGAGTCCCTGCGCAGAGGAGGCTGAGACCCGTTGCTTCCGAGATGAGAC 3780
QY 3781 ATTGAGGATTCCTCCATGACCCGACACCTACCAAGCTCTGTGACACACGACAGACA 3840
Db 3781 ATTGAGGATTCCTCCATGACCCGACACCTACCAAGCTCTGTGACACACGACAGACA 3840
QY 3841 CAGTGGAGATGAGTGGGCTGCGCTGAGAGGATTGACAGGATACAGAGGAGGATGAGAGAA 3900
Db 3841 CAGTGGAGATGAGTGGGCTGCGCTGAGAGGATTGACAGGATACAGAGGAGGATGAGAGAA 3900
QY 3901 AAGGAGCTTCACATCTAAAGGAGCTGACAGAACTGGCTGTGACGAGGACACACCTGA 3960
Db 3901 AAGGAGCTTCACATCTAAAGGAGCTGACAGAACTGGCTGTGACGAGGACACACCTGA 3960
QY 3961 GTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4020
Db 3961 GTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4020
QY 4021 CAGCGAGTATGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4080
Db 4021 CAGCGAGTATGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4080
QY 4081 GTGAGCTTCTTCACAGACCAACGACTACTAA 4111
Db 4081 GTGAGCTTCTTCACAGACCAACGACTACTAA 4111

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RESULT 3 US-08-340-011-1

Sequence 1: Application US/08340011
Patent No. 5776755

GENERAL INFORMATION:

APPLICANT: Alltalo, et al.
TITLE OF INVENTION: FIG. 4. A NOVEL RECEPTOR TYROSIN KINASE

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Korzun
STREET: 6300 Sears Tower, 213 South Wacker Drive

CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011

FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951

FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989

REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs

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? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 20..3916
US-08-340-011-1

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Query Match 95.2%; Score 3912.4; DB 1; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3913; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCACGGCCAGCCGCGGAGATGCAAGCGGGGCGGCGGCTGTGCTCGGAGCTGTGGCTCTG 60
Db 1 CCACGGCGAGCGCGCGGAGATGCAAGCGGGGCGGCGGCTGTGCTCGGAGCTGTGGCTCTG 60
QY 61 CTTGGGAGCTCTGAGAGCGGCTGTGGATGTGCTCTCATGACCCCGGACCTTGAAACAT 120
Db 61 CTTGGGAGCTCTGAGAGCGGCTGTGGATGTGCTCTCATGACCCCGGACCTTGAAACAT 120
QY 121 CAGGAGGAGATGACAGCTGATGACACCGGAGTGCACAGCTGTCATCTCTGAGGGAGACA 180
Db 121 CAGGAGGAGATGACAGCTGATGACACCGGAGTGCACAGCTGTCATCTCTGAGGGAGACA 180
QY 181 GCAACCCCTCGAGTGGCTTGGCTGAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 181 GCAACCCCTCGAGTGGCTTGGCTGAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
QY 241 CAGCGAGGAGACGGGGGGTGTGGAGACTCTGAGGGGACAGAGCGGAGGAGGAGGAGGAGGAG 300
Db 241 CAGCGAGGAGACGGGGGGTGTGGAGACTCTGAGGGGACAGAGCGGAGGAGGAGGAGGAGGAG 300
QY 301 GGTGTGCTGTGTCAGAGAGTACATGCAACAGACAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 301 GGTGTGCTGTGTCAGAGAGTACATGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 GTACATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
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QY 421 GTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 421 GTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 GTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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QY 661 GTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
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QY 721 GTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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QY	1441	CCGCGGGCGGACAGCAAGACCTCATGCTACAGTGGCGGTGACACAC	1500
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QY	1501	GCAGGATGGCGTGAACCCCATCGAGAGCTGGACACCTGGACGAGTTGTGGAGGAAA	1560
Db	1501	GCAGGATGCCGTGAACCCCATCGAGAGCTGGACACCTGGACGAGTTGTGGAGGAAA	1560
QY	1561	GAAATAGACTGTGAGCAAGCAAGCTGTGATCCAGATATCCAAAGCTGTGTGCATGTACAAAGTG	1620
Db	1561	GAAATAGACTGTGAGCAAGCAAGCTGTGATCCAGATATCCAAAGCTGTGTGCATGTACAAAGTG	1620
QY	1621	TGTGGTCTCCAAACAGGTGGGCCAGGATAGCGGCTCATTTACTTCTATGTGACACCAAT	1680
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QY	1681	CCCGAGCGGCTTACCATATCGATCGAAAGCAATCGAGAGACTATAGAGAGGCTACAGCGGT	1740
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QY	1741	GCTCTGAGCTGGCAAGCCGCAAGTATCAAGTAGCACCAATCGAGCTGGTACCCGCTCAA	1800
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QY	1801	CGTGTCCACGCTGACAGATGCGGCGAGGAGACCGCTGTCTGTGACTCAGAGAGCTGTGA	1860
Db	1801	CGTGTCCACGCTGACAGATGCGGCGAGGAGACCGCTGTCTGTGACTCAGAGAGCTGTGA	1860
QY	1861	TCGTGTGGCAGCCCTTGAGTGTGCGAGCTGAGAGAGCTGGCACTGTGGGTGCGTACAGC	1920
Db	1861	TCGTGTGGCAGCCCTTGAGTGTGCGAGCTGAGAGAGCTGGCACTGTGGGTGCGTACAGC	1920
QY	1921	CACGCTAGCGCTGAGTATCCCGCGCATTCGCGCGGACAGACAGAGGCCACATGTGTGGCA	1980
Db	1921	CACGCTAGCGCTGAGTATCCCGCGCATTCGCGCGGACAGACAGAGGCCACATGTGTGGCA	1980
QY	1981	ACTGCAAGACCGGCGACGCTATGACAAAGCATGCTCCACAGAAAGTACTGTGGGTGCAAGC	2040
Db	1981	ACTGCAAGACCGGCGACGCTATGACAAAGCATGCTCCACAGAAAGTACTGTGGGTGCAAGC	2040
QY	2041	CGTGAAGCCGCTGGGCTGACAGCAAGCTTGACCGACCTCTGTGGAGCTGAGGCACTG	2100
Db	2041	CGTGAAGCCGCTGGGCTGACAGCAAGCTTGACCGACCTCTGTGGAGCTGAGGCACTG	2100
QY	2101	GCCTGAGAAATGACAGTGTGTGGGAGCGAGCGACGCGGACGATGCTGTGTATCAAAAG	2160
Db	2101	GCCTGAGAAATGACAGTGTGTGGGAGCGAGCGACGCGGACGATGCTGTGTATCAAAAG	2160
QY	2161	CGAGAGGCTACTGTGAGAGGAAAAGTGTGAGTGCACCTTGGGAGCTCCAAACAGAAAGCTGAG	2220
Db	2161	CGAGAGGCTACTGTGAGAGGAAAAGTGTGAGTGCACCTTGGGAGCTCCAAACAGAAAGCTGAG	2220
QY	2221	CATCCAGCGGTGCGCGAGAGAGATGCTGAGAGCTGATCTGTGACGCTGTCCAAAGCCAA	2280
Db	2221	CATCCAGCGGTGCGCGAGAGAGATGCTGAGAGCTGATCTGTGAGCGGTGTCCAAAGCCAA	2280
QY	2281	GAGCGGCTCAACTCCGTCGACAGCGTGGCGTGTGAGAGGCTCCGAGAGATAGAGGCGACAT	2340
Db	2281	GAGCGGCTCAACTCCGTCGACAGCGTGGCGTGTGAGAGGCTCCGAGAGATAGAGGCGACAT	2340
QY	2341	GGAGATGATGATCTTGTGGGTAAGCGGCTGATGCTGCTTCTTCTGGGTCCCTCTCT	2400
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QY	2401	CCTCATCTCTGTAAACATGAGAGAGCGGCGCCACGAGACATAGAGAGGCGCTACTCTGTG	2460
Db	2401	CCTCATCTCTGTAAACATGAGAGAGCGGCGCCACGAGACATAGAGAGGCGCTACTCTGTG	2460
QY	2461	CATCATATATGAGACCCCGGAGAGGTGGCTGTGAGAGCAATATGCAATACGCTGTCTACGA	2520
Db	2461	CATCATATATGAGACCCCGGAGAGGTGGCTGTGAGAGCAATATGCAATACGCTGTCTACGA	2520
QY	2521	TACCAAGCAATGGGAAATTCUCCCGAAGAGCGGTCTGCATGTGGGAGAGAGCTTCGGCTACGG	2580

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 213 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent: Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-NOV-1994
CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/795,430
FILING DATE: 05-FEB-1997
APPLICATION NUMBER: PCI/F196/00427
FILING DATE: 01-AUG-1996
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/501,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLTYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-355-700-1:
Query Match 95.2% Score 3912.4 DB 4 Length 4416:
Host Local Similarity 100.0% Pired. No. 0:
Matches 3913: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 CCAAGCGGAGGAGGCGGAGATGACAGCGGAGGCGGCGCTGTCGCTGAGCTGCTG 60
DB 1 CCAAGCGGAGGAGGCGGAGATGACAGCGGAGGCGGCGCTGTCGCTGAGCTGCTG 60
QY 61 CCGTGGAGATGCTGAGAGGCTGAGTGGTACTGATGACCGCCCGAGCTTGAACAT 120
DB 61 CCGTGGAGATGCTGAGAGGCTGAGTGGTACTGATGACCGCCCGAGCTTGAACAT 120
QY 61 CCGTGGAGATGCTGAGAGGCTGAGTGGTACTGATGACCGCCCGAGCTTGAACAT 120
DB 61 CCGTGGAGATGCTGAGAGGCTGAGTGGTACTGATGACCGCCCGAGCTTGAACAT 120
QY 121 CAGAGGAGAGTACAGAGTATGAGAGCCGAGTACAGGCTGTCATCTGCTGAGGGACA 180
DB 121 CAGAGGAGAGTACAGAGTATGAGAGCCGAGTACAGGCTGTCATCTGCTGAGGGACA 180
QY 181 GCAAGGCTGCAATGAGGCTTGGGCGAGAGCTACAGAGGCGCTAGCTACCGAGAGACAGA 240
DB 181 GCAAGGCTGCAATGAGGCTTGGGCGAGAGCTACAGAGGCGCTAGCTACCGAGAGACAGA 240
QY 241 CAGAGGAGAGTACAGAGGCTGCTGAGAGTACAGAGGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 CAGAGGAGAGTACAGAGGCTGCTGAGAGTACAGAGGAGAGAGAGAGAGAGAGAGAGAG 300

QY 301 GGTGTGCTGCTGACAGAGTACATGCCAACACACAGAGAGAGTACGCTACTACAA 360
DB 301 GGTGTGCTGCTGACAGAGTACATGCCAACACACAGAGAGAGTACGCTACTACAA 360
QY 361 GTACATCAAGGACAGCATGAGAGGACACAGGCTGCGCAAGTCTAGCTGTTCAGAGA 420
DB 361 GTACATCAAGGACAGCATGAGAGGACACAGGCTGCGCAAGTCTAGCTGTTCAGAGA 420
QY 421 CTTTGAAGAGCATTCATCAACAAAGCTTACAGCTTGTGTCAACAGAGAGAGAGCAT 480
DB 421 CTTTGAAGAGCATTCATCAACAAAGCTTACAGCTTGTGTCAACAGAGAGAGAGCAT 480
QY 481 GTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 GTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 GGTGCTGTGGCCAGAGAGGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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QY 601 CAGGCGCATGCTGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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QY 661 CTTCTTTTCAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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QY 721 GTTCCCGAGAGAGT 780
DB 721 GTTCCCGAGAGAGT 780
QY 781 GTGGGCTGAGTTTACATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
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QY 841 GCGGGGTAAAGT 900
DB 841 GCGGGGTAAAGT 900
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DB 901 CCGTGGAGATGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 960
QY 961 CCGCATCCAGGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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QY 1261 GGAAGCTGT 1320
DB 1261 GGAAGCTGT 1320
QY 1321 CTACTGCGCTACAGCGGCGAGAGGCTGAGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 1380
DB 1321 CTACTGCGCTACAGCGGCGAGAGGCTGAGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 1380
QY 1381 CAGCATTCAGTGGCACTGGCGGCTTGGAGACAGCTGCAAGATGTTGGCCAGCGTAGCT 1440

Db	2461	CATATCATGAGAACCCCGGGGAGGTGGCTCTGGAGGAGCCAAATGGCAATACCTGTCTACGA	2520
OY	2521	TGCGACCGAGATGGGAATTTCCCGCGAGAGCGGCTGCACCTCGGGGAGATGCTGGGCTACGG	2580
Db	2521	TGGCACCGAGTGGGAATTTCCCGCGAGCGGCTGCACCTGGGGAGATGCTCTCGCTACGG	2580
OY	2581	CGCCTTGGGAAGGTGGTGAAGAGCTCCGTTTCGGCATTCACAAAGGGGACGACGTGGGA	2640
Db	2581	CGCCTTGGGGAAAGGTGGTGAAGAGCTTCGTTTCGGCATTCACAAAGGGGACGACGCTGGGA	2640
OY	2641	CACCTGGCCGTTGAAAAATGCTGAAGAGGGGCGCCACAGCGAGCAGCCGCGCTGAT	2700
Db	2641	CACCGTGGCCGTTGAAAAATGCTGAAGAGGGGCGCCACAGCGAGCAGCAGCAGCCGCGCTGAT	2700
OY	2701	GTGGAGAGCTCAAGATTCCTCATTGCATCGGCAACCACTCAAGTGGTCACTCTCGG	2760
Db	2701	GTGGAGAGCTCAAGATTCCTCATTGCATCGGCAACCACTCAAGTGGTCACTCTCTCGG	2760
OY	2761	GGCGTACCAACGCGCGAGGGGCCCCCTCATGATGATCGTGAAGTTCTTCGAATGACGGCA	2820
Db	2761	GGCGTACCAACGCGCGAGGGGCCCCCTCATGATGATCGTGAAGTTCTTCGAATGACGGCA	2820
OY	2821	CTCTCTCAACTCTCTGGGCGCTCAAGCGGGACGCTTCAGCCCTTGAGCGAGAGCTTCG	2880
Db	2821	CTCTCTCAACTCTCTGGGCGCGCAAGCGGGACCCCTTCAGCCCTTGAGCGAGAGCTTCG	2880
OY	2881	CGAGGAGCGCGGAGGCTTCGCGCGCATGATGGAGAGTGGCGCAGGTGGATTCGAGAGGTGCG	2940
Db	2881	CGAGGAGCGCGGAGGCTTCGCGCGCATGATGGAGAGTGGCGCAGGTGGATTCGAGAGGTGCG	2940
OY	2941	GGGCGACACGACGACGAGGTCTCTGTGCGCGGTTCTCGAAGCAGCGAGGGCGAGACGAGCG	3000
Db	2941	GGGCGACACGACGACGAGGTCTCTGTGCGCGGTTCTCGAAGCAGCGAGGGCGAGACGAGCG	3000
OY	3001	GGCTTCTCTCAGACCAAGAGCTGAGAGACCTGTGGCTGAGCCGCTGACCATGAGAGATCT	3060
Db	3001	GGCTTCTCTCAGACCAAGAGTGTAGAGACCTGTGGCTGAGCCGCTGACCATGAGAGATCT	3060
OY	3061	TGCTCTCTACACTTCCAGGTTGGAGGAGCAATGAGATGTTCTGCTTCCCGAAGATGAT	3120
Db	3061	TGCTCTCTACACTTCCAGGTTGGAGGAGCAATGAGATGTTCTGCTTCCCGAAGATGAT	3120
OY	3121	CCACAGACAGCTGGGCTGTGTGGAACTTCCTGCTGTGGAAAGCGACGTGGTGAAGATCG	3180
Db	3121	CCACAGAGACCTGGGCTGTGTGGAACTTCCTGCTGTGGAAAGCGACGTGTGAAGATCG	3180
OY	3181	TGACTTTGGGCTTGGCGGAGACATCTACAAACACCTGACTGACTCCGCAAGGGGCGTGC	3240
Db	3181	TGACTTTGGGCTTGGCGGAGACATCTACAAACACCTGACTGACTCCGCAAGGGGCGTGC	3240
OY	3241	CCGGCTGCCCTTGAAAGTGGATGGCCCTTAAAGCAATCTTCGCACAAAGGTGTACACACGA	3300
Db	3241	CCGGCTGCCCTTGAAAGTGGATGGCCCTTAAAGCAATCTTCGCACAAAGGTGTACACACGA	3300
OY	3301	GATGAGACGTGGTCTTTTGGGGTGTCTCTGGAGAACTTCTCTTGGGGGCTTCCG	3360
Db	3301	GATGAGACGTGGTCTTTTGGGGTGTCTCTGGAGAACTTCTCTTGGGGGCTTCCG	3360
OY	3361	GATGCCCTGGGATGATCATGAGAGGATTTCCGACGGGCTGAGAGGGGACCAAGGAT	3420
Db	3361	GATGCCCTGGGATGATCATGAGAGGATTTCCGACGGGCTGAGAGGGGACCAAGGAT	3420
OY	3421	GAGGGCCCGGAGCTGGGCACTCCCGCAATCGCCGATCATGCTGAACCTGCTGTCCG	3480
Db	3421	GAGGGCCCGGAGCTGGGCACTCCCGCAATCGCCGATCATGCTGAACCTGCTGTGTCG	3480
OY	3481	AGACCCCAAGGAGACCTGCATTCGAGAGTGTGGAGATCTCTGGGGAGCTGTGCA	3540
Db	3481	AGACCCCAAGGAGACCTGCATTCGAGAGTGTGGAGATCTCTGGGGAGCTGTGCA	3540
OY	3541	GGGCGAGGCTCTGCAAGAGAGAGGATTCGATGGCCCGCGAGCTCTTAAGAGCTC	3600
Db	3541	GGGCGAGGCTCTGCAAGAGAGAGGATTCGATGGCCCGCGAGCTCTTAAGAGCTC	3600

UY 1 CCACGCGCAGCGCGCGAGATC

GGAGATGCAGCGGGGCGCGCTGTCCCTGGCACTGTGGCTCTG 60

[illegible]

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1      FILINDATE: 4-APR-1994
2      CLASSIFICATION: 530
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: PCT/US93/00586
5      FILING DATE: 22-JAN-1993
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER: 07/826935
8      FILING DATE: 22-JAN-1992
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Lee, Wendy M.
11     REGISTRATION NUMBER:
12     REFERENCE/DOCKET INFORMATION:
13     TELECOMMUNICATION INFORMATION:
14     TELEPHONE: 415/225-1994
15     TELEFAX: 415/952-9881
16     TELEX: 910/371-7168
17     INFORMATION FOR SEQ ID NO: 31:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 4425 bases
20     TYPE: nucleic acid
21     STRANDEDNESS: single
22     TOPOLOGY: linear
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24     US-08-222-616-31
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QY	1381	CAGCATCCACTGGCACTGGGGGGCCCTGGAGACCCCTGGAGAGTGTGTTGGCCAGCGTAGTCT	1440
DB	1392	CAGATCCAGTGGCACTGGGGGGCCCTGGAGACCCCTGGAGAGTGTGTTGGCCAGCGTAGTCT	1451
QY	1441	CCGGCGGGGCGACAGCAAGACCTCATGTCCAGACGTGGCGGTGATCGTGAAGGGGGGTGACAC	1500
DB	1452	CCGGGGGGGGGACAGCAAGACCTCATGTCCAGACGTGGCGGTGATCGTGAAGGGGGGTGACAC	1511
QY	1501	GCAGGATGCGGCTGACACCCCATCGAGAGCCTGACACCTGGAGCGATTGTGAGGGAAA	1560
DB	1512	GCAGGATGCGGCTGACACCCCATCGAGAGCCTGACACCTGGAGCGATTGTGAGGGAAA	1571
QY	1561	GAAATAGACGTGTGAGCAAGCTGGTGGATCCAGAAATGCCAAAGTGTGTGGCATGTACAAAGT	1620
DB	1572	GAAATAGACGTGTGAGCAAGCTGGTGGATCCAGAAATGCCAAAGTGTGTGGCATGTACAAAGT	1631
QY	1621	TGTGGTCTCCAAACAGGTGGGCGCAGATAGCGGCTATCTACTTATGTATGTATCCCAT	1680
DB	1632	TGTGGTCTCCAAACAGGTGGGCGCAGATAGCGGCTATCTACTTATGTATGTATCCCAT	1691
QY	1681	CCCCGAGGGCTTCACCATCTGAATCCAAAGGCATCCGAGAGCACTACTATAGAGGGGCGACGGGT	1740
DB	1692	CCCCGAGGGCTTCACCATCTGAATCCAAAGGCATCCGAGAGCACTACTATAGAGGGGCGACGGGT	1751
QY	1741	GCTCTGAGCTGCCAAAGCGCCAGACTTACATAGTAGAGACATCTGGCTGTGATACCGGCTCAA	1800
DB	1752	GCTCTGAGCTGCCAAAGCGCCAGACTTACATAGTAGAGACATCTGGCTGTGATACCGGCTCAA	1811
QY	1801	CCTGTCCACGGCTGCAGATATGGCCACGAGAACCGGTTCTGTGTGACATCAAGAGCGTGTAT	1860
DB	1812	CCTGTTCACAGTTCGACATGTAGATGAGCAAGGAAACCGGTTGTGTGTGACATCAAGAGCGTGTAT	1871
QY	1861	TCTGTGTGCCACCCCTCTGTGGGCGGCGACGCTTGAGAGAGTGTGCAACCTGTGGGCGGCTGCAGCG	1920
DB	1872	TCTGTGTGCCACCCCTCTGTGGGCGGCGACGCTTGAGAGAGTGTGCAACCTGTGGGCGGCGCTGCAGCG	1931
QY	1921	CACGCTACGCTTAAATATCTCCCGCGCTCGCGCTCGGAGACAGAGAGCCCATATGTGTGGCA	1980
DB	1932	CACGCTACGCTTAAATATCTCCCGCGCTCGCGCTCGGAGAGACAGAGAGCCCATATGTGTGGCA	1991
QY	1981	AATGCAAAACCGGCGGAGCTCTGACAAAGCACTGCGCAAAAGATACCTGTGCGTGGAGGCG	2040
DB	1992	AATGCAAAACCGGCGGAGCTCTGACAAAGCACTGCGCAAAAGATACCTGTGCGTGGAGGCG	2051
QY	2041	CCTGGAAAGCTCTGTGCTACGAGCAAGATTGACCACTCTCTGCTGGAAAGCTGAGCGACATC	2100
DB	2052	CCTGGAAAGCTCTGTGCTACGAGCAAGATTGACCACTCTCTGCTGGAAAGCTGAGCGACATC	2111
QY	2101	CGTGGAAATGCAATGTGTGTGGGTGGGAGCGGACGCGCCGAGATCTGTGTGTATCAAGAA	2160
DB	2112	CGTGGAGATGCAATGTGTGTGGGTGGGAGCGGACGCGCCGAGATCTGTGTGTATCAAGAA	2171
QY	2161	CGAGAGGCTCTCTGGAAGAAAAAGTCTTGAGTGCACATCTGGCGAGCTCCAAACGAGAGTGA	2220
DB	2172	CGAGAGGCTCTCTGGAAGAAAAAGTCTTGAGTGCACATCTGGCGAGCTCCAAACGAGAGTGA	2231
QY	2221	CATCCAGTGGCTGGCGGAGAGAGATGCGGAGACCTATATCTGTGAGCGTGTGCACCGCCA	2280
DB	2232	CATCCAGTGGCTGGCGGAGAGAGATGCGGAGACCTATATCTGTGAGCGTGTGCACCGCCA	2291
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DB	2292	GGGCTGGCTCAATCTCTCGCGGACAGCTGGAGGCTCGAGAGGTATAGAGGCGAGT	2351
QY	2341	GGAGATCGTATCTTGTGGTACCGGCGTCACTGCGTCTTCTTCTGGGTCTCTCTCT	2400
DB	2352	GGAGATCGTATCTTGTGGTACCGGCGTCACTGCGTCTTCTTCTTCTGGGTCTCTCTCT	2411
QY	2401	CTCTCATCTCTGTGAATATAGAGAGCGTGGCGCGACGAGACATTAAGAGCGGCTCACTGTG	2460
DB	2412	CTCTCATCTCTGTGAATATAGAGAGCGTGGCGCGACATTAAGAGCGGCTCACTGTG	2471
QY	2461	CATATATCATGGACCCCGAGAGGTGTCTCTTGAGAGGAAATATGCAATACCTGTTCTTACA	2520

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Db 2832 GCGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 2891
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QY 3061 TGTCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3120
Db 3072 TGTCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3131
QY 3121 GCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3180
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Db 3252 GCGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3311
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Db 3492 AGAGCCAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3551
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Db 3552 GAGGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3611
QY 3601 AGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3660
Db 3612 AGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3671
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Db 3672 TGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3731
QY 3721 GTCTCTTCCGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3780
Db 3732 GTCTCTTCCGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3791
QY 3781 ATTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3840
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QY 3841 CAGTGGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAG 3900
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QY 3901 AAGCGCTTCAAGT 3914
Db 3912 AAGCGCTTCAAGT 3925

RESULT 10
PCT-US95-04228-31
Sequence 31, Application PCT/US9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Shao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-Apr-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/971-7168
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

PCT-US95-04228-31

Query Match 95.2% Score 3912.4 DB 5 Length 4425;
Best Local Similarity 100.0% Pref. No. 0
Matches 3913; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACGCCGACGCGCGGAGATGACAGCGGCGCGCGCTGCTGCGACAGTGGCTCTG 60
DB 12 CCACGCCGACGCGCGGAGATGACAGCGGCGCGCGCTGCTGCGACAGTGGCTCTG 71
QY 61 CCGGAGCTCTGCTGAGCGGCTGCTGAGTGGCTATGCTGATGACGCTGCGGACCTTGAACAT 120
DB 72 CCGGAGCTCTGCTGAGCGGCTGCTGAGTGGCTATGCTGATGACGCTGCGGACCTTGAACAT 131
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DB 132 CAGCGAGAGTACAGAGTTCATGAGACAGCGGAGCGGCTGCTGATCTCTGCGAGGAGCA 191
QY 181 GCAACCGCTGAGAGTGGCTGCGAGAGAGTTCAGAGAGCGCGGACCGGACCGGACAGCA 240
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QY 361 GATACATGAGAGTTCATGAGAGTTCATGAGAGTGGCTGCGAGAGAGTTCAGAGAGCGGCT 420
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DB 432 CTTGAGAGTTCATGAGAGTTCATGAGAGTGGCTGCGAGAGAGTTCAGAGAGCGGCT 491
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DB 492 GTCGCTGCTGCTGAGAGTTCATGAGAGTGGCTGCGAGAGAGTTCAGAGAGCGGCT 551
QY 541 GTCGCTGCTGCTGAGAGTTCATGAGAGTGGCTGCGAGAGAGTTCAGAGAGCGGCT 600
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DB 1872 TCGCTGCGAGAGTTCATGAGAGTTCATGAGAGTGGCTGCGAGAGAGTTCAGAGAGCGGCT 1931
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[illegible]

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Qy	3421	GAGGGCCCCGGAGACTGGCCACTGCCGCCATACGCCGATCTATGTGTAACCTGTGTGCGG	3480
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Qy	3541	GGGCAAGGGCCCTCTCAAGAGGAAGAGAGTCTGACATGGCCCGGCGACCTCTCAGAGCTC	3600
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Qy	3601	ACAAAGAGGAGACTTCTGCAAGGTGTCACACATGGACCTACATCGCCACAGGTGACCC	3660
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Qy	3661	TGAGGACAGCCCGCCAGACCTGCAGCGCCACAGCCTGAGCGCGAGGTAATTACAATGGGT	3720
Db	3672	TGAGGACAGCCCGCCAGACCTGCAGCGCCACAGCCTGAGCGCGAGGTAATTACAATGGGT	3731
Qy	3721	GTCCCTTCCTCCGGGCTGTCTGTGCGAGAGGGCTTGAGACCCGTGGTCTCTCCAGATGAAAGC	3780
Db	3732	GTCCCTTCCTCCGGGCTGTCTGTGCGAGAGGGCTTGAGACCCGTGGTCTCTCCAGATGAAAGC	3791
Qy	3781	ATTGAGAGAAATTCCTCATGACCCCAACGACCTACAAAGCTCTGTGGACCAACGACGACA	3840
Db	3792	ATTGAGAGAAATTCCTCATGACCCCAACGACCTACAAAGCTCTGTGGACCAACGACGACA	3851
Qy	3841	CAGTGGAGATGGTCTGGCCTTGAGAGAGTTTGAGCAATAGAGAGAGGCATATACAGACA	3900
Db	3852	CAGTGGAGATGGTCTGGCCTTGAGAGAGTTTGAGCAATAGAGAGAGGCATATACAGACA	3911
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Db	3912	AAGCGGCTTCAGGCT 3925	

RESULT 11
 US-08-446-648-45
 Sequence 45, Application US/08446648
 Patent No. 6331302
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Bennett, Brian D.
 APPLICANT: Goeddel, David
 APPLICANT: Lee, James M.
 APPLICANT: Matthews, William
 APPLICANT: Tsai, Siao Ping
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE ACONIST ANTIBODIES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080


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Db 2624 CCGGATGAGGCTCACCATGGAATCCAGGACATCCGAGGAGCTGTAGAGGGCCAGCCGGT 2683
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QY 1861 TCTGTGGCCAGCCCTCTGTGGCCGACGCTGGAGGAGGTGGCACTGGGGGCGCGCACGC 1920
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Db 2984 CCTGGAAGCCCTGAGCTCAGCTAGAGATGAGGAGCTGCTGCTGTAAGCTGAGGAGCTC 2100
QY 2101 GCTGGAAGTSCAGCTGCTTGGTGCGCGAGCCGACGCGCCGAGCATGCTGTGCTACAAAGA 2160
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QY 2161 GAGAGAGCTGCTGAGAGGAAAGTCTGAGTGAATGAGTGGAGCTCCAGCCAGAGCTGAG 2220
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Db 3164 CATGAGAGCTGCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
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Db 3224 GAGCTGAGTCAACCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
QY 2341 GAGAGTGTGATCTTGTGAGTACCGAGGAGTATGAGTGTCTTGTGAGTGTCTCTCT 2400
Db 3284 GAGAGTGTGATCTTGTGAGTACCGAGGAGTATGAGTGTCTTGTGAGTGTCTCTCT 2400
QY 2401 GCTGCACTTCTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Db 3344 GCTGCACTTCTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
QY 2461 CATATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Db 3404 CATATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 2521 TGCCAGGAGTGGAGATTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
Db 3464 TGCCAGGAGTGGAGATTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
QY 2581 GAGCTTGGAGAGAGTGGAGAGCTCCGCTTTCGCGATTCAGAGAGAGAGAGAGAG 2640
Db 3524 GAGCTTGGAGAGAGTGGAGAGCTCCGCTTTCGCGATTCAGAGAGAGAGAGAGAG 2640
QY 2641 CAGCGTGGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
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QY 2701 GCTGAGAGTTCAGATCTATTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760
Db 3644 GCTGAGAGTTCAGATCTATTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760
QY 2761 GAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
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QY 2821 CCTTCGAACCTTCTGCGGCGCCAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
Db 3764 CCTTCGAACCTTCTGCGGCGCCAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 2881 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
Db 3824 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
QY 2941 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
Db 3884 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
QY 3001 GAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
Db 3944 GAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060
QY 3061 TGTCTGTACAGCTTCCAGGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
Db 4004 TGTCTGTACAGCTTCCAGGTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
QY 3121 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
Db 4064 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3180
QY 3181 TGACTTTGAGCTTGGCGGAGATCTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240
Db 4124 TGACTTTGAGCTTGGCGGAGATCTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240
QY 3241 CCGGCTGCGCTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3300
Db 4184 CCGGCTGCGCTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3300
QY 3301 GAGTGAAGTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
Db 4244 GAGTGAAGTGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
QY 3361 GTACCTTGGAGTGTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
Db 4304 GTACCTTGGAGTGTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420
QY 3421 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
Db 4364 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
QY 3481 AGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540
Db 4424 AGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3540
QY 3541 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
Db 4484 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3600
QY 3601 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
Db 4544 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
QY 3661 TAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3720
Db 4604 TAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3720
QY 3721 GTCCTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
Db 4664 GTCCTTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
QY 3781 ATTGAGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840
Db 4724 ATTGAGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840
QY 3841 CAGTGGAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
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QY 3746 GGGGCTGAGACCCGCTCTCTCCAGGATGAACATTTGACCAATTCOCATGACCCCA 3805
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 QY 3806 AGGAGCTGACAAAGCTCTCTGAGCAACGAGTACATATGAGATGCTGAGCTCGGAG 3865
 DB 1987 AGGAGCTGACAAAGCTCTCTGAGCAACGAGTACATATGAGATGCTGAGCTCGGAG 1928
 QY 3866 GAGTTGAGATAGAGAGAGGAGATGAGCAAGAAAGGCTTCAGCT 3914
 DB 1927 GAGTTGAGATAGAGAGAGGAGATGAGCAAGAAAGGCTTCAGCT 1879

RESULT 14

US-09-446-648-17/c
 Sequence 17, Application US/09446648
 Patent No. 6333302

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
 APPLICANT: Benmelt, Brian D.
 APPLICANT: Goeddel, David
 APPLICANT: Lee, James M.
 APPLICANT: Matthews, William
 APPLICANT: Tsai, Siao Ping
 APPLICANT: Wood, William J.
 TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatix (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/446,648
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/222616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 49,378
 REFERENCE/DOCKET NUMBER: P0821P3HCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6827 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear

Query Match 25.38; Score 1040.2; DB 4; Length 6827;
 Best local Similarity 98.18; Pred. No. 4.6e-202;
 Matches 1051; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2846 GAGGAGGCTTCAGGAGGCTGCGGAGAGAGTCCCGGAGCAGGCGGAGCGCTTCGCGGC 2905
 DB 2947 GAGGAGGCTTCAGGAGGCTGCGGAGAGAGTCCCGGAGCAGGCGGAGCGCTTCGCGGC 2888
 QY 2906 ATGGTGAGCTGCGGAGGCTGATGAGAGCGGCGGAGAGGAGAGGAGGCTTCCTTTT 2965
 DB 2887 ATGGTGAGCTGCGGAGGCTGATGAGAGCGGCGGAGAGGAGAGGAGGAGGCTTCCTTTC 2828

QY 2966 GCGGCTTCGCGGAGGAGGCGGAGGAGGAGGCGGCGCTTCGAGACCCAGAAAGCTGAG 3025
 DB 2827 GCGGCTTCGCGGAGGAGGCGGAGGAGGAGGAGGCGCTTCGAGACCCAGAAAGCTGAG 2768
 QY 3026 GAGCTGTGGCTGAGGCGGCTGAGACCAATGGAAGATCTTGTGCTACAGCTTCGAGTGGCC 3085
 DB 2767 GAGCTGTGGCTGAGGCGGCTGAGACCAATGGAAGATCTTGTGCTACAGCTTCGAGTGGCC 2708
 QY 3086 AGAGGAGATGAGATTCTGAGCTGCGGAGAGTGCATCCAGAGAGCTGCTGAGAG 3145
 DB 2707 AGAGGAGATGAGATTCTGAGCTGCGGAGAGTGCATCCAGAGAGCTGCTGAGAG 2648
 QY 3146 ATTCTGTGCTGCGGAGGAGGAGGAGTGTGGAAGATCTGTGACTTTGGCTTCGCGGAGATG 3205
 DB 2647 ATTCTGTGCTGCGGAGGAGGAGGAGTGTGGAAGATCTGTGACTTTGGCTTCGCGGAGATG 2588
 QY 3206 TACAAAGAGGCTGAGTACGTCGCGGAGGAGGAGTGCCTGCGGCTGAGAGTGAATGAG 3265
 DB 2587 TACAAAGAGGCTGAGTACGTCGCGGAGGAGGAGTGCCTGCGGCTGAGAGTGAATGAG 2528
 QY 3266 CCTGAAGAGATCTTCGAGCAAGGTTGACACAGGAGTGAAGCTGTGATTTGGGGT 3325
 DB 2527 CCTGAAGAGATCTTCGAGCAAGGTTGACACAGGAGTGAAGCTGTGATTTGGGGT 2468
 QY 3326 CTTCCTGGGAGAGATCTTCTCTCTGAGGAGGCTGAGGAGTGAAGCTGTGATTTGGGGT 3385
 DB 2467 CTTCCTGGGAGAGATCTTCTCTCTGAGGAGGCTGAGGAGTGAAGCTGTGATTTGGGGT 2408
 QY 3386 GAGTTGAGGAGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3445
 DB 2407 GAGTTGAGGAGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2348
 QY 3446 GCGATAGGCGGATCATGCTGAAATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3505
 DB 2347 GCGATAGGCGGATCATGCTGAAATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2288
 QY 3506 TGGAGGCTGGGAGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3565
 DB 2287 TGGAGGCTGGGAGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2228
 QY 3566 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3625
 DB 2227 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2168
 QY 3626 TCCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3685
 DB 2167 TCCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2108
 QY 3686 GCGCAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3745
 DB 2107 GCGCAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2048
 QY 3746 GGGGCTGAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3805
 DB 2047 GGGGCTGAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1988
 QY 3806 AGGAGCTTACAAAGGCTCTGTGAGCAACGAGACATAGTGGATGCTGCTGAGCTCGGAG 3865
 DB 1987 AGGAGCTTACAAAGGCTCTGTGAGCAACGAGACATAGTGGATGCTGCTGAGCTCGGAG 1928
 QY 3866 GAGTTGAGATAGAGAGAGGAGATGAGCAAGAAAGGCTTCAGCT 3914
 DB 1927 GAGTTGAGATAGAGAGAGGAGATGAGCAAGAAAGGCTTCAGCT 1879

RESULT 15

PCT-US95-04228-17/c
 Sequence 17, Application PC/TUS9504228

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
 APPLICANT: Benmelt, Brian D.
 APPLICANT: Goeddel, David


```
location/Qualifiers
1. .603
/organism="Homo sapiens"
```

Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory

Db 546 ATGTGGGAGGGCTGTCGTCATCCCGGCTCAATGTCACGCTGGC 598

BASE COUNT	225 a	195 c	232 g	183 t
CRISIN				

RESULT 15
B0604389/c

FEATURES

SOURCE

Query Match	6.98;	Score 284.6;	DB 14;	Length 697;
Best local Similarity	65.68;	Pred. NO. 3.4e-47;		
Matches 432; Conservative	0;	Mismatches 224;	Indels 3;	Gaps 1

QY	2213	AAAGTCGACATCCAGGCGCTGCGCGAGAGAGATGCGGAGCGCATCTGTGCGAGCGGTGCG	2272
Db	695	AGCGTGTATTATTGAAAGAGTACGCGAAGAGAGATGAAAGCGGCTGTATCTACCTGACGAGCCACG	636
QY	2273	AAAGCGCAAGGCGCGGTCAACTCTCTCCGCAACCTGGCGCTGTGAAAGCTCCGAGGATTAAG	2333
Db	635	AAACGAAAGGAGGTCCGCGAAGCTGGGATACCTCAACCTGCAAGAAAGCTCGGAAAG	576
QY	2333	GGCAGCATGGAGATCGTATCTGTCCGCTACCGGCGTCATCGCTGTCTTCTTGCGATC	2392
Db	575	TTCAGGCTGAGGTGATCAACCTGAGGTGACTGTGTGGCTGCAACCTCTTCTGATC	516
QY	2392	CTCCTCTCTCTATCTTTCTGTAACTGAGGAGCGGCGCCACCGCAAGCATTAAGATAGCGC	2455
Db	515	CTGCTAAACCTCTTTATCCGAAAGTGAAGAGGCTTCTTCTGATGATTAAGCTGAC	459

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QY 2453 TACCTGTCATCATCATGAGACCCCGGAGAGTGGCTGTGAGAGCAATGCGATTACCTG 2512
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 TACCTGTCATCATCATGAGACCCCGGAGAGTGGCTGTGAGAGCAATGCGATTACCTG 399
QY 2513 TCTTACGATGCCAGCCCATGAGGAATTCCCGGAGAGGAGCTGTACCTGAGGAGAGTGGCTG 2572
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 CTTTACGATGCCAGCCCATGAGGAATTGGCTGTGAGAGCAATGCGATTACCTG 339
QY 2573 GAGCTACGGGAGCTTGGGAGAGTGGTGAAGCTTGTGGCTTCCGATCCAGAGGGCAGC 2632
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 338 GGAAGAGGGGCTTTTGGGAAAGTGGTCCAGAGCACTGGCTTTGGCTATTAGAAATCACC 279
QY 2633 AGCTGTGACACGCTGGCGGTGAAATGCTTAAAGAGAGAGGAGGAGGAGGAGGAGCAGC 2692
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 278 AGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 219
QY 2693 GGGCTGATGTGAGAGCTGAGATGCTCATTGACATGAGGAGGAGGAGGAGGAGGAGGAG 2752
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 GTCCTGATGACTGAGCTGAGATCTTACCCAGATGAGGAGGAGGAGGAGGAGGAGGAG 159
QY 2753 CTTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2812
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 158 CTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 99
QY 2813 TACGAGACCTGTCGAACTTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2871
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98 TATGTAATTTATCGAAGTACCTCAAGAGCAAGCGAGCTTATTCTTCATCAACAAGA 40
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Search completed: May 1, 2003, 10:56:35
Job time : 5053 secs

DR WPI; 2000-679298/66.
DR P-PSUB; AAB29047.

XX Screening a human subject for increased risk of developing a lymphatic
 PT disorder, comprises assaying a nucleic acid to determine a mutation
 PT altering the sequence of a vascular endothelial growth factor
 receptor-3 -

PS Claim 14: Page 46-52: 76pp. English.

XX The present sequence is the coding sequence for the human vascular
 CC endothelial growth factor receptor 3 (VEGFR-3, also known as Flt4 or
 CC fms-like tyrosine kinase 4). It was used in the methods of the invention,
 CC which involve the screening of individuals to determine which VEGFR-3
 CC alleles they possess and thus their likelihood of developing hereditary
 CC lymphoedema. Conditions associated with lymphoedema include Milroy's
 CC syndrome, which is early onset lymphoedema and lymphoedema praecox, which
 CC is late onset.

XX Sequence 4111 BP: 846 A: 1273 C: 1298 G: 694 T: 0 other:

Query Match 100.0% Score 4111: DB 21: Length 4111:

Best Local Similarity 100.0%: Pct. No. 0: Mismatches 0: Indels 0: Gaps 0:

Matches 4111: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 1 CCAGCCGACACGCGCGAGATGACAGCGGGGCGCGCGCTGTGCTGCACTGTGCTCTG 60
 DB 1 CCAGCGACAGCGCGCGAGATGACAGCGGGGCGCGCGCTGTGCTGCACTGTGCTCTG 60
 QY 6: CCTGGACCTCTGTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
 DB 61 CTTGGACCTCTGTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
 QY 121 CACGAGAGATGACAGCTGATGACAGCGGGGCGCGCGCTGTGCTGCACTGTGCTCTG 180
 DB 121 CACGAGAGATGACAGCTGATGACAGCGGGGCGCGCGCTGTGCTGCACTGTGCTCTG 180
 QY 121 CACGAGAGATGACAGCTGATGACAGCGGGGCGCGCGCTGTGCTGCACTGTGCTCTG 180
 DB 121 CACGAGAGATGACAGCTGATGACAGCGGGGCGCGCGCTGTGCTGCACTGTGCTCTG 180
 QY 181 GCACCTCTGTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 DB 181 GCACCTCTGTGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 QY 241 CAGGAGAGATGAGCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 DB 241 CAGGAGAGATGAGCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 QY 301 GGT 360
 DB 301 GGT 360
 QY 361 GTATATGAGAGAGATGAGCGGACACCGCGCGCTGTGCTGCACTGTGCTCTG 420
 DB 361 GTATATGAGAGAGATGAGCGGACACCGCGCGCTGTGCTGCACTGTGCTCTG 420
 QY 421 CTTGAGAGAGATGATGAGAGCTGTGATGAGCTGTGATGAGAGAGAGAGAGAG 480
 DB 421 CTTGAGAGAGATGATGAGAGCTGTGATGAGCTGTGATGAGAGAGAGAGAGAG 480
 QY 481 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 481 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB 541 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 QY 601 CACGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 601 CACGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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 DB 661 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
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 DB 721 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

DB 721 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 QY 781 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 781 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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 DB 841 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 QY 901 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB 901 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
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 DB 961 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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 DB 1021 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 1081 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 DB 1081 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 QY 1141 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 DB 1141 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 QY 1201 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1261 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1261 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 QY 1321 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 DB 1321 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 QY 1381 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
 DB 1381 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
 QY 1441 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 DB 1441 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 QY 1501 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 DB 1501 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 QY 1561 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 DB 1561 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 QY 1621 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
 DB 1621 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
 QY 1681 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 DB 1681 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 QY 1741 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
 DB 1741 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
 QY 1801 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
 DB 1801 GTGGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860

QY	2941	CGGAGACGACGACGAGGTCCTCTTCGCGCGGTTCTCGAAGACCGAGGGCGAGCGAGGCG	3000
DB	2941	GGGAGACGAGGAGAGGGTCTCTTCGCGCGGTTCTCGAAGACCGAGGGCGAGGCGAGGCG	3000
QY	3001	GGCTTCCGAGACCAAGAGCTGAGAGACCTGTGGTGAACCCGCTGACATGSAATCT	3060
DB	3001	GGCTTCCGAGACCAAGAGACCTGTGGTGAACCCGCTGACATGSAATCT	3060
QY	3061	TGTTCTACAGCTCCAGAGTGGCCACAGGGATGAGATTCCGGCTTCCGAAAGTGCAT	3120
DB	3061	TGTTCTACAGCTCCAGAGTGGCCACAGGGATGAGATTCCGGCTTCCGAAAGTGCAT	3120
QY	3121	CCACAGAGACCTGGCTGCTCGGAACTTGTGCTGCGAAGGCAAGTGGTGAATGCG	3180
DB	3121	CCACAGAGACCTGGCTGCTCGGAACTTGTGCTGCGAAGGCAAGTGGTGAATGCG	3180
QY	3181	TGACTTTGGGCTTGCCCGGGACATCTCCAAAGACCTGACTAGCTCGCAAGGGCATGCG	3240
DB	3181	TGACTTTGGGCTTGCCCGGGACATCTCCAAAGACCTGACTAGCTCGCAAGGGCATGCG	3240
QY	3241	CCGGCTCCCGTGAAGTGGATGCGCTGAAACATCTTGCGAAGGTGTACATCGACGCA	3300
DB	3241	CCGGCTCCCGTGAAGTGGATGCGCTGAAACATCTTGCGAAGGTGTACATCGACGCA	3300
QY	3301	GACTGACGTGTGGTCCCTTGGGGTGCTTCTGTGGAGATCTCTCTGTGGGGCTCTGCC	3360
DB	3301	GACTGACGTGTGGTCCCTTGGGGTGCTTCTGTGGAGATCTCTCTGTGGGGCTCTGCC	3360
QY	3361	GTAACCTGGGGTGCAGATCAATGAGAGATTCTCCAGTGGCTGAGAGACGGCACAGCAT	3420
DB	3361	GTAACCTGGGGTGCAGATCAATGAGAGATTCTCCAGTGGCTGAGAGACGGCACAGCAT	3420
QY	3421	GAGGGCCCGGAGCGGGCCATCTCCGCAATAGCGGCAATGCTGAACTGCTGGTCCG	3480
DB	3421	GAGGGCCCGGAGCGGGCCATCTCCGCAATAGCGGCAATGCTGAACTGCTGGTCCG	3480
QY	3481	AGACCCCAAGCGAGACCTGCACTCTCTGAGACCTGATGGAGATCTGGGGAGACTGTGTCA	3540
DB	3481	AGACCCCAAGCGAGACCTGCACTCTCTGAGACCTGATGGAGATCTGGGGAGACTGTGTCA	3540
QY	3541	GGGAGGGGCTGTGCAAGAGAAAGAGAGGTCTGCATGGCTGGCGAGCTGTGAGAGTC	3600
DB	3541	GGGAGGGGCTGTGCAAGAGAAAGAGAGGTCTGCATGGCTGGCGAGCTGTGAGAGTC	3600
QY	3601	AGAAAGGGGCACTTCTGTGGAGGTGTGCACATGAGGCTTACACATGCGCCAGCTACGCG	3660
DB	3601	AGAAAGGGGCACTTCTGTGGAGGTGTGCACATGAGGCTTACACATGCGCCAGCTACGCG	3660
QY	3661	TGAGGACACCGCGCAAGCTGTGAGAGCTGAGAGCTGGCGCCAGTATTACACATGGGT	3720
DB	3661	TGAGGACACCGCGCAAGCTGTGAGAGCTGAGAGCTGGCGCCAGTATTACACATGGGT	3720
QY	3721	GTCCTTCCCGGGTCCCTGTGGCTGAGAGGGGTTCAGACCCGTGTCTCTCCAGATGAGAG	3780
DB	3721	GTCCTTCCCGGGTCCCTGTGGCTGAGAGGGGTTCAGACCCGTGTCTCTCCAGATGAGAG	3780
QY	3781	ATTGAGGAATTCGCCATGACCTGTCAAGATCTACAAAGGCTCTGTGACAACTGACAGCA	3840
DB	3781	ATTGAGGAATTCGCCATGACCTGTCAAGATCTACAAAGGCTCTGTGACAACTGACAGCA	3840
QY	3841	CAGTGGAGTGTGTGGGCTCTCGAGAGAGTTTACAGACATAGAGAGCGGCATAGACAGA	3900
DB	3841	CAGTGGAGTGTGTGGGCTCTCGAGAGAGTTTACAGACATAGAGAGCGGCATAGACAGA	3900
QY	3901	AAGGGCTTCAGCTGTAAAGACCTGAGCAGAAATGTGGCTGTGACAGGGCACACCTTGA	3960
DB	3901	AAGGGCTTCAGCTGTAAAGACCTGAGCAGAAATGTGGCTGTGACAGGGCACACCTTGA	3960
QY	3961	CTTCCCAAGGAGAGCGGGCGGGCTTAAATGGGGGGCCCGAAGAGGCTAGGTGTTTACAA	4020
DB	3961	CTTCCCAAGGAGAGCGGGCGGGCTTAAATGGGGGGCCCGAAGAGGCTAGGTGTTTACAA	4020
QY	4021	CAGCGAGTATGGGAGCTGTGTGAGGCAAGCGAGAGAGACCATGCTCCCGCTGTGGCGG	4080

QY	2101	GGTGGAAATCAACATGCTTGGTGGGCGGAGCCGACCGCCGCTCGAGATCTGTGGTATCAAA	2160
Db	2101	GGTGGAGATCAATGCTTGGTGGGCGGAGCGGACCGCCGCTCGAGATCTGTGGTATCAAA	2160
QY	2161	GCAGAGGCTCTCGAGAGAAAAAGTCTGAGTGCATTTGGCGGACTCCAAACGAGAGTGG	2220
Db	2161	GCAGAGGCTCTCGAGAGAAAAAGTCTGAGTGCATTTGGCGGAGTCCAAACGAGAGTGG	2220
QY	2221	CATCCACGGGTGGCGAGAGAGATGAGGAGCGATATCTGTGACGTGTCCAAAGCTCA	2280
Db	2221	CATCCACGGGTGGCGAGAGAGATGAGGAGCGATATCTGTGAGGTGTCCAAAGCTCA	2280
QY	2281	GGCGTGGGTCAACTCTCTCGGACACCGTGGGTCTGGAAAGGCTCGAGAGTAAGGGGACAT	2340
Db	2281	GGCGTGGGTCAACTCTCTCGGACACCGTGGGTCTGGAAAGGCTCGAGAGTAAGGGGACAT	2340
QY	2341	GGAGATGCTGATCTCTTGTCGGTACCGGGCTCATGCTGTCTTCTTGGGTCTCTCTCT	2400
Db	2341	GGAGATGCTGATCTCTTGTCGGTACCGGGCTCATGCTGTCTTCTTGGGTCTCTCTCT	2400
QY	2401	CGCATCTCTCTTAACATGAGAGAGGCCGCGCTCAGCGAGATATAGAGCGGCTACTCTTC	2460
Db	2401	CGCATCTCTCTTAACATGAGAGAGGCCGCGCTCAGCGAGATATAGAGCGGCTACTCTTC	2460
QY	2461	CATCATATGAGACCCCGGGGAGCGCTCTGTGGAGACATGCGAATACCTTGTCTTACGA	2520
Db	2461	CATCATATGAGACCCCGGGGAGCGCTCTGTGGAGACATATGCGAATACCTTGTCTTACGA	2520
QY	2521	TGCCAGCCAGTGGGAAATTCGCCGAGAGCGGCTGACCTGGGAGAGTGTCTGCGCTACGCG	2580
Db	2521	TGCCAGCCAGTGGGAAATTCGCCGAGAGCGGCTGACCTGGGAGAGTGTCTGCGCTACGCG	2580
QY	2581	CGCCTCTGGGAAAGTGTGTGGAGAGCTTCGCGCTTGTGGCATCAAGGGCAGCAGCTGTGA	2640
Db	2581	CGCCTCTGGGAAAGTGTGTGGAGAGCTTCGCGCTTGTGGCATCAAGGGCAGCAGCTGTGA	2640
QY	2641	CACGGTGGCGCTGAAAAATGCTGAAAGAGGGGCCGACGGCCAGTGAAGACCGCGCGTGTAT	2700
Db	2641	CACGGTGGCGCTGAAAAATGCTGAAAGAGGGGCCGACGGCCAGGAGACCGCGCGCTGTAT	2700
QY	2701	GTCGGAGCTCAGATCTCATTTCAATCTGCGCAACCCACTCAAGTGTGTCAACTCTCTCGG	2760
Db	2701	GTCGGAGCTCAGATCTCATTTCAATCTGCGCAACCCACTCAAGTGTGTCAACTCTCTCGG	2760
QY	2761	GGCGTGCACCAAGCCGGCAGGGGCCCTCTCATGGTATGTGTGAGTTCTCAAGTACGGCAA	2820
Db	2761	GGCGTGCACCAAGCCGGCAGGGGCCCTCTCATGGTATGTGTGAGTTCTCAAGTACGGCAA	2820
QY	2821	CGCTCTCCAACTCTCTGCGCGCGCAAGGGGAGACCCCTTAGCGCCCTCGCGGAGAAATCTCC	2880
Db	2821	CGCTCTCCAACTCTCTGCGCGCGCAAGGGGAGACCCCTTAGCGCCCTCGCGGAGAAATCTCC	2880
QY	2881	CGAGCAGCGCGACGCTTCGAGCCCATGCTGTGAGACTCGCGAGCTGATCGAGGCGGCGC	2940
Db	2881	CGAGCAGCGCGGACGCTTCGAGCCCATGCTGTGAGACTCGCGAGCTGATCGAGGCGGCGC	2940
QY	2941	GGGAGAGAGAGAGAGGCTCTTCTGCGCGGCTTCTGAAACCGGAGGGCGGAGCGAGCTG	3000
Db	2941	GGGAGAGAGAGAGAGGCTCTTCTGCGCGGCTTCTGCAAAACCGGAGGGCGGAGCGAGCTG	3000
QY	3001	GGCTTCTTCAGACCAAGAGTGAAGACTGTGGCTAGCGCGCTCGACATGAGAACATCT	3060
Db	3001	GGCTTCTTCAGACCAAGAGTGAAGACTGTGGCTAGCGCGCGCTCGACATGAGAACATCT	3060
QY	3061	TGCTGCTACAGCTTCCAGGTGGCCAGAGGAGTGGATTTCTTGCTTCCCGAAAGTGCAT	3120
Db	3061	TGCTGCTACAGCTTCCAGGTGGCCAGAGGAGTGGATTTCTTGCTTCCCGAAAGTGCAT	3120
QY	3121	CCACAGAGACCTGGCTGCTCGGAAACATTTCTGCTGTGGAAAGCGAGCGTGGTGAAGATCTG	3180
Db	3121	CCACAGAGACCTGGCTGCTCGGAAACATTTCTGCTGTGGAAAGCGAGCGTGGTGAAGATCTG	3180

QY	181	GCACCCCTCTGAGTGGCTTGTGCGACAGACTTACGACAGCGCCACGCCACCCGAGACACGA	240
DG	181	GCACCCCTCTGAGTGGCTTGTGCGACAGACTTACGACAGCGCCACGCCACCCGAGACACGA	240
QY	241	CAGCAGACACACAGGATGGTGGAGATATCGAGAGATACAGAGCGCCAGCCCTACTGAGA	300
DG	241	CAGCAGACACACAGGATGGTGGAGATATCGAGAGATACAGAGCGCCAGCCCTACTGAGA	300
QY	361	GATGTTGCTGCTTCACAGAGTACATGCCACAGACACAGGAGTACGTTGCTACTACAA	360
DG	361	GATGTTGCTGCTTCACAGAGTACATGCCACAGACACAGGAGTACGTTGCTACTACAA	360
QY	421	CTTTGAGTACCTATATCAACAAGCTTACACGCTTTTGATCAACAAGAAAGACCCAT	480
DG	421	CTTTGAGTACCTATATCAACAAGCTTACACGCTTTTGATCAACAAGAAAGACCCAT	480
QY	481	GTGGTGGCTGTGTGTGATCTCCCGGCTCAATGTACGCTCGCCTGCAAAAGCTC	540
DG	481	GTGGTGGCTGTGTGTGATCTCCCGGCTCAATGTACGCTCGCCTGCAAAAGCTC	540
QY	541	GATGCTGTGCGCAGACAGCGACAGAGTGTGAGGATGACAGCGCGGCGGATGCTGGTGC	600
DG	541	GATGCTGTGCGCAGACAGCGACAGAGTGTGAGGATGACAGCGCGGCGGATGCTGGTGC	600
QY	601	CAGCGCACCTGCTGACAGATATGCCGTGACCTGCAGATGCGAAGCTACCTGGGAGACGAGA	660
DG	601	CAGCGCACCTGCTGACAGATATGCCGTGACCTGCAGATGCGAAGCTACCTGGGAGACGAGA	660
QY	661	CTTCTCTTCAACCCCTCTCTGGTGTGACATACACAGGTAACGAGCTCTATGACATCCAGCT	720
DG	661	CTTCTCTTCAACCCCTCTCTGGTGTGACATACACAGGTAACGAGCTCTATGACATCCAGCT	720
QY	721	GTATGACAGAGAGTGTGTGAGGCTGCTGTGTGATGAGGAGCAACGCTGCTGAACTGACGCT	780
DG	721	GTATGACAGAGAGTGTGTGAGGCTGCTGTGTGATGAGGAGCAACGCTGCTGAACTGACGCT	780
QY	781	GTGGCTGAGGTTTAACTAGAGTGTACGCTTTGACTGGGATACCCAGGGAAGGAGCGACA	840
DG	781	GTGGCTGAGGTTTAACTAGAGTGTACGCTTTGACTGGGATACCCAGGGAAGGAGCGACA	840
QY	841	GGGGGGTAAGTGGTGGCCAGAGGAGGCTGCCAGCATACCCACAGAACTCTCCAGCAT	900
DG	841	GGGGGGTAAGTGGTGGCCAGAGGAGGCTGCCAGCATACCCACAGAACTCTCCAGCAT	900
QY	901	CGTAGGATATCAAGAGTGTACGCCAGCAGCAGCTGGGTGTGATATGTGTGCAAGGCCAACAA	960
DG	901	CGTAGGATATCAAGAGTGTACGCCAGCAGCAGCTGGGTGTGATATGTGTGCAAGGCCAACAA	960
QY	961	CGGCAATCCAGAGGTTTGGAGAGAGACCGCAGGTATTTGTGATGAAAATCCCTTCAAG	1020
DG	961	CGGCAATCCAGAGGTTTGGAGAGAGACCGCAGGTATTTGTGATGAAAATCCCTTCAAG	1020
QY	1021	GGTGGATGAGTCAAGAGGACCCATCTGTGAGAGCAGAGGACAGAGCAGCGTGGTGAAGCT	1080
DG	1021	GGTGGATGAGTCAAGAGGACCCATCTGTGAGAGCAGAGGACAGAGCAGCGTGGTGAAGCT	1080
QY	1081	GCCCGTAAAGTGTGAGAGGTACGCCCGCCCGCCAGTTCCAGTGGTATCAAGGATGGAAGGC	1140
DG	1081	GCCCGTAAAGTGTGAGAGGTACGCCCGCCCGCCAGTTCCAGTGGTATCAAGGATGGAAGGC	1140
QY	1141	ACTGTGCGGGCCCGACATCCATCCCTGCTGCTTAAGAGGTGAGACAGAGCCGACGAC	1200
DG	1141	ACTGTGCGGGCCCGACATCCATCCCTGCTGCTTAAGAGGTGAGACAGAGCCGACGAC	1200
QY	1201	AGGCAAGCTACACCTTCGCTCTGTGGAATCTGGCTGCTGAGGCGCAACATCAGCTT	1260
DG	1201	AGGCAAGCTACACCTTCGCTCTGTGGAATCTGGCTGCTGAGGCGCAACATCAGCTT	1260

OY	1261	GGAGCTGGTGGTGAATGGCGCCCGCCCGGAGTACATGAAAGAGAGCCCTCTCTCCCGAAGAT	1320
Db	1261	GGAGCTGGTGGTGAATGGCGCCCGCCCGGAGTACATGAAAGAGAGCCCTCTCTCCCGAAGAT	1320
OY	1321	CTACTGGCCTCAACAGCCAGCCAGCCCTCACTACGTGCACGGCCCTACGAGGATGCTCTCTCTCT	1380
Db	1321	CTACTGGCCTCAACAGCCAGCCAGCCCTCACTACGTGCACGGCCCTACGAGGATGCTCTCTCTCT	1380
OY	1381	CAGCATTCAGTGGCACTGGCGGCCCTGGACACCCCTGCAGATGTTTGGCCAGCGTAGCT	1440
Db	1381	CAGCATTCAGTGGCACTGGCGGCCCTGGACACCCCTGCAGATGTTTGGCCAGCGTAGCT	1440
OY	1441	CGGGGGGGGGGAGGAGGAGCAAGCACTCTATGGCCATAGTGGCGCTGTACTGAGAGGGCGGTACAC	1500
Db	1441	CGGGGGGGGGGAGGAGGAGCAAGCACTCTATGGCCATAGTGGCGCTGTACTGAGAGGGCGGTACAC	1500
OY	1501	GCAGGATGGCTGTGAACCCCATCTCAGAGATCTGTACACCTGTGCACAGGATTTGTGGAGGAAA	1560
Db	1501	GCAGGATGGCGGTGAACCCCATCTCAGAGATCTGTACACCTGTGTACAGGATTTGTGGAGGAAA	1560
OY	1561	GAAATAGACTGTGAGCAAGCTGTGTATTCAGATGCCAAGTGTGTGCCATGTACAAATG	1620
Db	1561	GAAATAGACTGTGAGCAAGCTGTGTATTCAGATGCCAAGTGTGTGCCATGTACAAATG	1620
OY	1621	TGTGGCTTCACAAAGAGTGGGGCCAGCATATAGGGCTCATCTACTTCTATGTACACCATAT	1680
Db	1621	TGTGGCTTCACAAAGAGTGGGGCCAGCATATAGGGCTCATCTACTTCTATGTACACCATAT	1680
OY	1681	CCCCGAGGCTTCACACATCGAATGCAAGCCATCGAGAGCTACTAGAGGTCACAGGTCACATGGGT	1740
Db	1681	CCCCGAGGCTTCACACATCGAATGCAAGCCATCGAGAGTCTATAGAGGTCACAGGTCACATGGGT	1740
OY	1741	GCTCCTGAGCTGCGCAAGCCGACACAGCTTACAGTACAGACATCTCGCTGTGTACCGCTCTCAA	1800
Db	1741	GCTCCTGAGCTGCGCAAGCCGACACAGCTTACAGTACAGACATCTCGCTGTGTACCGCTCTCAA	1800
OY	1801	CGTGTCCACACCTGTGCACCATGTGCACAGGAGAACCCGCTTCTGTCTGACTGTGCAGAACGTGCA	1860
Db	1801	CGTGTCCACACCTGTGCACCATGTGCACAGGAGAACCCGCTTCTGTCTGACTGTGCAGAACGTGCA	1860
OY	1861	TCTGTTGCGCACCCCTCTGCGCCGCGCTGTGAGAGAGTGGCACTGTGGGGCGCGCCACAGC	1920
Db	1861	TCTGTTGCGCACCCCTCTGCGCCGCGCTGTGAGAGAGTGGCACTGTGGGGCGCGCCACAGC	1920
OY	1921	CAGGCTCAAGCTGAGTATCCCGCGCGTCCGCGCCGAGACAGAGAGGCCACTATGTGTGGA	1980
Db	1921	CAGGCTCAAGCTGAGTATCCCGCGCGTCCGCGCCGAGACAGAGAGGCCACTATGTGTGGA	1980
OY	1981	AGTGCAGAACGCGCGCGCACCATATACAAAGACACTGTGCACAGAAATACCTGTGGGTGCAGGC	2040
Db	1981	AGTGCAGAACGCGCGCGCACCATATACAAAGACACTGTGCACAGAAATACCTGTGGGTGCAGGC	2040
OY	2041	CGTGAAGCCCTCTGGCTCAACCGCAGAACTTGACGCACTCTGTGTGATGACGTACAGCGACTC	2100
Db	2041	CGTGAAGCCCTCTGGCTCAACCGCAGAACTTGACGCACTCTGTGTGATGACGTACAGCGACTC	2100
OY	2101	GCTGGAGATGCAGTCTTGTGGCTCGAGAGCACGCGCGCCAGCATGTTGTGTACAAAGA	2160
Db	2101	GCTGGAGATGCAGTCTTGTGGCTCGAGAGCACGCGCGCCAGCATGTTGTGTACAAAGA	2160
OY	2161	CGAGAGGCTGTGCGAGGAAAAAGTCTGTAGATTCACATTGGCGGACTCTCCAAACCAAACTGAG	2220
Db	2161	CGAGAGGCTGTGCGAGGAAAAAGTCTGTAGATTCACATTGGCGGACTCTCCAAACCAAACTGAG	2220
OY	2221	CATTCAGGCGCTGTGGCGGAGGAGATCCGCGACCGCTATCTGTGCAGGGTGTGCACGCCAA	2280
Db	2221	CATTCAGGCGCGTGTGGCGGAGGAGATCCGCGACCGCTATCTGTGCAGGGTGTGCACGCCAA	2280
OY	2281	GGGCTCGTCACTCTCTCCGCGACGCTGGCGCTGTGAAAGCTCTCCAGAGATTAAGGAGAGCAT	2340
Db	2281	GGGCTCGTCACTCTCTCCGCGACGCTGGCGCTGTGAAAGCTCTCCAGAGATTAAGGAGAGCAT	2340
OY	2341	GGAGATGTGATCTCTTCGGTACCGCGCTCATCGCTCTCTCTGGGCTCTCTCTCT	2400

Db	3421	GAAGGCCCCGAGCTGGCCACTCCCGCATACCGCCGCATCATCTGTAATCTCTGTCCGG	3480
OY	3481	AGACCCCAAGGCCAGACGCTGCTATTTCTGGAGCTGTGTAGATCTCTGGGGACCTGGCTCA	3540
Db	3481	AGACCCCAAGGCCAGACGCTGGATTTCTGGAGCTGTGTAGATCTCTGGGGACCTGGCTCA	3540
OY	3541	GGGCAAGGGGCTCTCAAGAGAAAGAGAGGCTGTGCATGGCCCCGGGCACTCTTCACAGCTC	3600
Db	3541	GGGCAAGGGGCTCTCAAGAGAAAGAGAGGCTGTGCATGGCCCCGGGCACTCTTCAGAGCTC	3600
OY	3601	AGAGAGAGGAGAGCTTCTGGCAGAGTGTCCACCAATGGCCCTACACATGGCCAGAGTACAGC	3660
Db	3601	AGAGAGAGGAGAGCTTCTGGCAGAGTGTCCACCAATGGCCCTACACATGGCCAGAGTACAGC	3660
OY	3661	TGAGGACACGCCGCCCAAGCTGTGCAGGCCACACAGCTTGCGCTAGGTAATTACAACTGGGT	3720
Db	3661	TGAGGACACGCCGCCCAAGCTGTGCAGGCCACACAGCTTGCGCCAGGTAATTACAACTGGGT	3720
OY	3721	GTCTCTTCCGGGCTGGCTGGCCCAAGGAGGCTGACACCCGCTGGTCTCCAGCATGAGAGC	3780
Db	3721	GTCTCTTCCGGGCTGGCTGGCCCAAGGAGGCTGACACCCGCTGGTCTCCAGCATGAGAGC	3780
OY	3781	ATTTCAGGAATTCCTCCATACGCTCCCAACGACCTACAAAGCTCTGTGGACCAACGACAGA	3840
Db	3781	ATTTCAGGAATTCCTCCATACGCTCCCAACGACCTACAAAGCTCTGTGGACCAACGACAGA	3840
OY	3841	CAGTGGAGTGTCTGGCTGGAGGAGGTTGTAGCAGATGAGAGAGGCAATGACAAAG	3900
Db	3841	CAGTGGAGTGTCTGGCTGGAGGAGGTTGTAGCAGATGAGAGAGGCAATGAGCAAGAA	3900
OY	3901	AAGCGGCTTCAGCTGTAAAGAGACCTGGCCAGAAATGTGGCTGTACAGAGGACACCTGA	3960
Db	3901	AAGCGGCTTCAGCTGTAAAGAGACCTGGCCAGAAATGTGGCTGTACAGAGGACACCTGA	3960
OY	3961	CTCCCAAGGAGAGCGCGCGCGGCTCAGCGGGGGGCTCCGAGAGGCGCAAGTGTTCACA	4020
Db	3961	CTCCCAAGGAGAGCGCGCGCGGCTCAGCGGGGGGCTCCGAGAGGCGCAAGTGTTCACA	4020
OY	4021	CAGCAGATGAGGGAGAGCTGTGGAGGCTAAGGACAGAGAGACCACTGTCGCCGCTGCCG	4080
Db	4021	CAGCAGATGAGGGAGAGCTGTGGAGGCTAAGGACAGAGAGAGACCACTGTCGCCGCTGCCG	4080
OY	4081	CGTGACCTTCTTCCACGACCAACAGACTACTAA	4111
Db	4081	CGTGACCTTCTTCCACGACCAACAGACTACTAA	4111
RESULTS 4			
AAC68952			
ID	AAC68952 standard; cDNA: 4111 bp.		
AC	AAC68952;		
XX	27-FEB-2001 (first entry)		
DE	Human FLT4/VEGFR-3 coding sequence.		
XX	Human; gene therapy; lymphatic disorder; hereditary lymphoedema; FLT4;		
XX	vascular endothelial growth factor receptor 3; VEGFR-3; VEGF-C; VEGF-D;		
XX	fms-like tyrosine kinase 4; ss.		
XX	Homo sapiens.		
XX	Key		
FT	CDS	Location/Qualifiers	
FT		20..4111	
FT		/tag= a	
FT		/product= "Human FLT4/VEGFR-3"	
XX	CA2283470-A1.		
XX	26-SEP-2003.		
XX	29-SEP-1999.		
XX	99CA-2283470.		

XX 26-MAR-1999: 99MO-US06133.
PR 16-AUG-1999: 99US-0375248.
XX
PA (UPEI-) UNIV PITTSBURGH.
PA (UPEI-) UNIV HELSINKI LICENSING LTD OY.
PA (UPEI-) LUDWIG INST CANCER RES.
XX
PI Alitalo K, Ferrell RE, Finogov DN, Karkkainen M.
XX WPI: 2001-007762/02.
DR P-PSDB: AAB37604.
XX
PT Screening a human for an increased risk of developing lymphatic
disorder comprises assaying nucleic acid for alterations in the
sequences expressing vascular endothelial growth factor receptor-3.
XX
PS Claim 15: Pages 48-54; 99pp; English.
XX
CC The present invention relates to a method for screening a human subject
for an increased risk of developing a lymphatic disorder e.g. hereditary
lymphoedema. The method comprises assaying nucleic acid of a human
subject to determine a presence or an absence of a mutation altering the
sequence or expression of vascular endothelial growth factor receptor-3
(VEGFR-3)/flms-like tyrosine kinase 4 (Flt4) allele and determining an
increased risk of developing lymphatic disorder from presence or absence
of the mutation. The present sequence is the coding sequence for human
VEGFR-3/Flt4. The presence of a mutation altering the encoded amino acid
sequence or expression of at least 1 VEGFR-3 allele in the nucleic acid
correlates with an increased risk of developing a lymphatic disorder.
CC Treatment for hereditary lymphoedema can be provided through the
administration of VEGF-C and VEGF-D genes (via gene therapy) and
proteins.
XX
SQ Sequence 4111 BF: 846 A; 1272 C; 1295 G; 694 I; 0 other:
Query Match 100.0%; Score 4109.4; DB 22; Length 4111;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 GCACGCGCAAGCGCGGAGATGACAGCGGCGCGCGCGCTGTCGACAGTGGCTG 60
DB 1 GCACGCGCAAGCGCGGAGATGACAGCGGCGCGCGCGCTGTCGACAGTGGCTG 60
QY 61 CCGTGGACTGCTGGAGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
DB 61 CCGTGGACTGCTGGAGCGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 CACGAGAGATGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
DB 121 CACGAGAGATGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 180
QY 181 GCACGCGCAAGCGCGGAGATGACAGCGGCGCGCGCGCTGTCGACAGTGGCTG 240
DB 181 GCACGCGCAAGCGCGGAGATGACAGCGGCGCGCGCGCTGTCGACAGTGGCTG 240
QY 241 CAGCGAGAGACGCGGCGGCTGGTGGAGACTGGAGGCGACAGAGCGCGCGCGCTG 300
DB 241 CAGCGAGAGACGCGGCGGCTGGTGGAGACTGGAGGCGACAGAGCGCGCGCGCTG 300
QY 301 GGTGGTGGTGGTGGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
DB 301 GGTGGTGGTGGTGGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
QY 361 GTACATCAAGGACAGCATGGAGGACACAGCGCGCGCGCTGTCGACAGTGGCTG 420
DB 361 GTACATCAAGGACAGCATGGAGGACACAGCGCGCGCGCTGTCGACAGTGGCTG 420
QY 421 GTTGGAGAGAGATGACAGTGGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGAG 480
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DB 601 CAGCGCACTGCTGGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
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DB 661 GTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 720
QY 721 GTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
DB 721 GTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
QY 781 GTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
DB 781 GTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
QY 841 GCGGGGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
DB 841 GCGGGGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 900
QY 901 CCTGACATCCACAACTGACGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
DB 901 CCTGACATCCACAACTGACGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
QY 961 CCGCATCCAGCATTTTGGGAGAGACCGCAGAGTGGTGGTGGTGGTGGTGGTGG 1020
DB 961 CCGCATCCAGCATTTTGGGAGAGACCGCAGAGTGGTGGTGGTGGTGGTGGTGG 1020
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DB 1021 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080
QY 1081 GCGCGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140
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QY 1141 ACTGTGGGCGGCGCACAGTGCACATGCTGGTGGTGGTGGTGGTGGTGGTGG 1200
DB 1141 ACTGTGGGCGGCGCACAGTGCACATGCTGGTGGTGGTGGTGGTGGTGGTGG 1200
QY 1201 AGGCACTACAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1260
DB 1201 AGGCACTACAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1260
QY 1261 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1320
DB 1261 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1320
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DB 1321 CTACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1380
QY 1381 CAGCATCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1440
DB 1381 CAGCATCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1440
QY 1441 CCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1500
DB 1441 CCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1500
QY 1501 GCGAGATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1560
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D0 721 GTTCCCAAGAGTGGTGGAGTGTGTGTAGAGGAGAGTGGTGTCTGAACTGCACCGT 780
QY 781 GTGGCGTGAATTAATCAGTGTACACTTTGACTGGGAGTACCCAGGAGAGGACAGA 840
DB 781 GTGGCGTGAATTAATCAGTGTACACTTTGACTGGGAGTACCCAGGAGAGGACAGA 840
QY 841 GAGGCGTGAATGGTGGTGGAGGAGCGGTGGCAGCAGAGCCAGCAGAGTCTTCAGCAT 900
DB 841 GCGGCGTGAATGGTGGTGGAGGAGCGGTGGCAGCAGAGCCAGCAGAGTCTTCAGCAT 900
QY 901 CTGGACCATTCAGAGTGCAGCGAGCAGCGCTGGGCTGTATGTGTGCAAGGCCAACA 960
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QY 961 CGGATTCAGAGCATTTGGGAGAGCAGCGAGTCTGATGATGAATTCCTTCATCAG 1020
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QY 1021 GTTGGAGTGGCTTGAAGAGGCTCATCTGTGAAGGCGAGGAGAGAGTGTGAAGCT 1080
DB 1021 GTTGGAGTGGCTTGAAGAGGAGCTCATCTGTGAAGGCGAGGAGAGAGTGTGAAGCT 1080
QY 1081 GCGCGTGAAGGAGAGTGGTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1140
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QY 1141 ACTGTCCCGGCGCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1200
DB 1141 ACTGTCCCGGCGCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1200
QY 1201 AGTGTACATACATCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
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QY 1261 GGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1320
DB 1261 GGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1320
QY 1321 CTATGAGCTCAGAGCGCCAGCGCCCTGACCTGACCTGACCTGACCTGACCTGACCT 1380
DB 1321 CTATGAGCTCAGAGCGCCAGCGCCCTGACCTGACCTGACCTGACCTGACCTGACCT 1380
QY 1381 CAGTATCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1440
DB 1381 CAGTATCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1440
QY 1441 GCGGCGGCGGCGAGAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1500
DB 1441 GCGGCGGCGGCGAGAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1500
QY 1501 GCAAGGATGCGGAGAGCGGATGCAAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1560
DB 1501 GCAAGGATGCGGAGAGCGGATGCAAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1560
QY 1561 GAATAGACTGTGAGCAGAGTGTGATGCAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1620
DB 1561 GAATAGACTGTGAGCAGAGTGTGATGCAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1620
QY 1621 TGTTGTGTCAGAGTGGTGGGCGAGATGAGCGGCTCATCTACTTCTATGTGAGCAGCAT 1680
DB 1621 TGTTGTGTCAGAGTGGTGGGCGAGATGAGCGGCTCATCTACTTCTATGTGAGCAGCAT 1680
QY 1681 GCGGCGGCGGCTTACCATGATCAGAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1740
DB 1681 GCGGCGGCGGCTTACCATGATCAGAGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1740
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QY 1801 GCTGTGAGTGTGCAAGCGAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1860
DB 1801 GCTGTGAGTGTGCAAGCGAGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 1860
QY 1861 TGTGTTGCGCACCGCTGTGGCGGAGCGCTGAGAGAGTGGACCTGGGGCGCGCCAGCG 1920
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QY 1921 CAGCTCAGCTGAGTATCCCGCGGTGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
DB 1921 CAGCTCAGCTGAGTATCCCGCGGTGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
QY 1981 AGTGCAG 2040
DB 1981 AGTGCAG 2040
QY 2041 CTTGAG 2100
DB 2041 CTTGAG 2100
QY 2101 GCTGAG 2160
DB 2101 GCTGAG 2160
QY 2161 GAG 2220
DB 2161 GAG 2220
QY 2221 CATCAG 2280
DB 2221 CATCAG 2280
QY 2281 GGGCTGTGCTACCTCTCGGCGAGCGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2340
DB 2281 GGGCTGTGCTACCTCTCGGCGAGCGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2340
QY 2341 GGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2400
DB 2341 GGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2400
QY 2401 CTTATCTTCTGTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
DB 2401 CTTATCTTCTGTATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
QY 2461 CATCATCATGAG 2520
DB 2461 CATCATCATGAG 2520
QY 2521 TGGCAG 2580
DB 2521 TGGCAG 2580
QY 2581 GCGCTTGGGAG 2640
DB 2581 GCGCTTGGGAG 2640
QY 2641 CAGCTGTGGGAG 2700
DB 2641 CAGCTGTGGGAG 2700
QY 2701 GTCGAG 2760
DB 2701 GTCGAG 2760
QY 2761 GGGCTGTGAG 2820
DB 2761 GGGCTGTGAG 2820
QY 2821 CTTCTCCAACTTCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
DB 2821 CTTCTCCAACTTCTGCGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 2881 GAG 2940
DB 2881 GAG 2940

PT	nucleic acid probes - used to diagnose and treat e.g. metastatic
PR	cancers, involving alterations to lymphatic vessels.
XX	
PS	Claim 9; Page 27-33; 54pp; English.
CC	A DNA sequence (AatII2068) coding for FLT4 receptor tyrosine kinase
CC	(AAP0528) is used as a probe that specifically binds/hybridizes to
CC	DNA encoding human FLT4. Such probes are used to detect FLT4, a
CC	novel marker for lymphatic vessels and some high endothelial
CC	veinules, in biological tissue for use in diagnosis and therapy of
CC	e.g. inflammatory, infectious and immunological diseases, metastatic
CC	lymph nodes and lymphangiomata.
SQ	Sequence 4195 BP; 889 A; 1278 C; 1305 G; 723 T; 0 other:
	Query Match 95.1%; Score 3910.8; DB 17; Length 4195;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 3912; Conservative 0; Mismatches 2; Indels 0; Gaps
OY	1 CCACGGCAGCGCCGCGAGATGCAGCGCGGCCCTGTGCTGCACATGTGGTCTG 60
DB	1 CCACGGCAGCGCGCGAGATGCAGCGCGGCCCTGTGCTGCACATGTGGTCTG 60
OY	61 CCTGGGACTCTTCGACCGCCCTGTGATGCTCACTACGCCCCCGACTTTGAACAT 120
DB	61 CCTGGGACTCTTCGACCGCCCTGTGATGCTCACTACGCCCCCGACTTTGAACAT 120
OY	121 CACGGAGAGATCACAGCTCATGACACCGGATGACAGCTGTGCATCTCTCTACAGGACA 180
DB	121 CACGGAGAGATCACAGCTCATGACACCGGATGACAGCTGTGCATCTCTCTACAGGACA 180
OY	181 GCACCCCCCTCGAGTGGGCTTGCCAGGAGCTCAGAGAGGCCACCACCGGATACAAAGA 240
DB	181 GCACCCCCCTCGAGTGGGCTTGCCAGGAGCTCAGAGAGGCCACCACCGGATACAAAGA 240
OY	241 CACCGAGACACCGGGGGTGTGTGAGACTGTGGACAGGACAGAGCCGCTTAGTCAA 300
DB	241 CACCGAGACACCGGGGGTGTGTGAGACTGTGGACAGGACAGAGCCGCTTAGTCAA 300
OY	301 GGATGTGCTGTGTGACAGAGTAATCCACAGACAGAGAGGATATGCTCTACTACAA 360
DB	301 GGATGTGCTGTGTGACAGAGTAATCCACAGACAGAGAGGATATGCTCTACTACAA 360
OY	361 GTACATCAAGGACAGCATGGAGGGACACACGGCCGCCAGCTCTTACGTGTCTGACAGA 420
DB	361 GTACATCAAGGACAGCATGGAGGGACACACGGCCGCCAGCTCTTACGTGTCTGACAGA 420
OY	421 CTITGGAGGCATTATCAACAAGATGACAGGCTTTGGTAAACAGAGAGAGAGAG 480
DB	421 CTITGGAGGCATTATCAACAAGATGACAGGCTTTGGTAAACAGAGAGAGAGAG 480
OY	481 GTGGGTGCTGTGTGTGATGTCATATCCGGGCTTAATGTACAGCTGTGCTGTAAACCTG 540
DB	481 GTGGGTGCTGTGTGTGATGTCATATCCGGGCTTAATGTACAGCTGTGCTGTAAACCTG 540
OY	541 GGAGCTGTGGCCAACAGCGGACAGAGTGGTGTGGAGTGAACCGGCGGAGCATGCTCGTGTG 600
DB	541 GGAGCTGTGGCCAACAGCGGACAGAGTGGTGTGGAGTGAACCGGCGGAGCATGCTCGTGTG 600
OY	601 CACGGCATTGTGTGACATGCCCTGTACTGTGATGTGGAGACACACTGTGGAGACACAGA 660
DB	601 CACGGCATTGTGTGACATGCCCTGTACTGTGATGTGGAGACACACTGTGGAGACACAGA 660
OY	661 CTTCCTTTCAACCCCTTCTGTGATCATAATCAGGACAGAGACTCTATGACATCCAGCT 720
DB	661 CTTCCTTTCAACCCCTTCTGTGATCATAATCAGGACAGAGACTCTATGACATCCAGCT 720
OY	721 GTTGGCCAGGAGTGGCTGGAGCTGTGTGAGGGAGAAAGAGTGTGCTGGAAGTGTGACAGCT 780
DB	721 GTTGGCCAGGAGTGGCTGGAGCTGTGTGAGGGAGAAAGAGTGTGCTGGAAGTGTGACAGCT 780
OY	781 GTGGGCTAGTATTAACTCAGTGCTGACTTTGACATGGGACTACCCAGGGAAGTAGGACAGA 840
DB	781 GTGGGCTAGTATTAACTCAGTGCTGACTTTGACATGGGACTACCCAGGGAAGTAGGACAGA 840


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Db 2521 GACGAGAGTGGCTGGACCTGGGAGAGTGGCTGGCTACAGGCGCTTGGGAGAGTGGT 2580
QY 2600 GAAGCTTCGGCTTTGGGATCCACAGGCGACACCTGGACACCTGGCGCTGAAAATG 2659
Db 2581 GAGGCTTCGGCTTTGGGATCCACAGGCGAGAGCTGGACACCTGGCGCTGAAAATG 2640
QY 2660 CTGAAGAGAGGCGCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2719
Db 2641 CTGAAGAGAGGCGCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2700
QY 2720 ATTCAATCGGACACCACTCAAGCTGATACCTTCTGCGGAGGAGGAGGAGGAGGAGGAG 2779
Db 2701 ATTCAATCGGACACCACTCAAGCTGATACCTTCTGCGGAGGAGGAGGAGGAGGAGGAG 2760
QY 2780 GCGCGCGCTGATGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2839
Db 2761 GCGCGCGCTGATGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820
QY 2840 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2899
Db 2821 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2880
QY 2900 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2959
Db 2881 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2940
QY 2960 CTCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3019
Db 2941 CTCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3000
QY 3020 GCTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3079
Db 3001 GCTTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3060
QY 3080 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3139
Db 3061 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3120
QY 3140 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3199
Db 3121 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3180
QY 3200 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3259
Db 3181 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3240
QY 3260 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3319
Db 3241 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3300
QY 3320 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3379
Db 3301 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3360
QY 3380 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3439
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QY 3440 ACTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3499
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QY 3500 GCAATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3559
Db 3481 GCAATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3540
QY 3560 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3619
Db 3541 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
QY 3620 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3679
Db 3601 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3660

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QY 3680 CTGACGCGGACACAGGCTGGCGCGGAGATATACAACTGGTGTCTTTCGGGAGTGGCTG 3739
Db 3661 CTGACGCGGACACAGGCTGGCGCGGAGATATACAACTGGTGTCTTTCGGGAGTGGCTG 3720
QY 3740 GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3799
Db 3721 GCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3780
QY 3800 ACCCAACGACCTACAAAGGCTCTGTGGACACCAAGACAGACAGTGGATGTCTGGCC 3859
Db 3781 ACCCAACGACCTACAAAGGCTCTGTGGACACCAAGACAGACAGTGGATGTCTGGCC 3840
QY 3860 TCGGAGGAGTGTGACAGATAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3914
Db 3841 TCGGAGGAGTGTGACAGATAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3895

RESULT 11
AAC62210
ID AAC62210 standard; DNA; 4450 BP.
XX
AC AAC62210:
XX
DT 06-MAR-2001 (first entry)
XX
DE Nucleotide sequence of the human flt-4 gene.
XX
KM Antisense oligonucleotide: flt-4; receptor type tyrosine kinase;
KM Lymphangiogenesis; prostate cancer; prostate cell; ss.
XX
OS Homo sapiens.
XX
PH Key 22.3918
FT CDS
FT
FT location/qualifiers
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FT /*tag_a
FT /product="flt-4"
FT /transl_except- (pos: 55..57, aa: Trp)
FT /transl_except- (pos: 58..60, aa: Leu)
FT /transl_except- (pos: 61..63, aa: Cys)
FT /transl_except- (pos: 64..66, aa: Leu)
FT /transl_except- (pos: 67..69, aa: Gly)
FT /transl_except- (pos: 70..72, aa: Leu)
FT /transl_except- (pos: 73..75, aa: Leu)
FT /transl_except- (pos: 76..78, aa: Asp)
FT /transl_except- (pos: 79..81, aa: Gly)
FT /transl_except- (pos: 82..84, aa: Val)
FT /transl_except- (pos: 85..87, aa: Ser)
FT /transl_except- (pos: 88..90, aa: Ser)
FT /transl_except- (pos: 91..93, aa: Asp)
FT /transl_except- (pos: 94..96, aa: Tyr)
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FT /transl_except- (pos: 1639..1641, aa: Lys)
FT /transl_except- (pos: 2236..2238, aa: Arg)
FT /transl_except- (pos: 3508..3510, aa: Ser)
FT /transl_except- (pos: 3598..3600, aa: Ser)
FT /transl_except- (pos: 3796..3798, aa: Phe)

W020062063-A1.
XX
PD 19-OCT-2000.
XX
PF 13-APR-1999: 99MO-US08079.
XX
PR 13-APR-1999: 99MO-US08079.
XX
PA (NMBl-) NORTHWEST BIOTHERAPEUTICS INC.
XX
PI Su SL.
XX
DR WPI: 2000-667067/67.
DR P-PSDB: AAB10542.
XX

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AC AA049753;
 XX
 DI 10-MAR-1994 (first entry)
 XX
 DE PTK gene SAL-S1.
 XX
 KW PTK; protein tyrosine kinase; catalytic domain; c-kit; FLT/FLK;
 KW fetal liver kinase; megakaryocyte; amplification; primer;
 KW polymerase chain reaction; PCR; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key location/qualifiers
 FH CDS complement (1877..2923)
 FT /*tag- a
 FT misc_difference 3026
 FT /*tag- b
 FT /*note- "base labelled as X in the specification"
 FT /*tag- c
 FT /*note- "base illegible in the specification"
 FT misc_difference 5693..5700
 FT /*tag- d
 FT /*note- "bases illegible in the specification"
 XX
 FN W0315201-A.
 XX
 DI 05-AUG-1993.
 XX
 PE 22-JAN-1993; 93MD-0500586.
 XX
 PR 22-JAN-1992; 92US-0826935.
 XX
 FA (NEML-) NEW ENGLAND DEACOMFSS HOSPITAL.
 XX
 PI Avraham H, Cowley S, Groopman J, Scadden D;
 XX
 DR WPI: 1993-120336/40.
 XX
 DR P-FSDB; AA041540.
 XX
 PI New protein tyrosine kinase genes and proteins encoded by genes -
 PT are of human mega-karyocytic origin
 XX
 PS Claim 2: fig 4; 60pp; English.
 XX
 CC PTK genes were identified using two sets of degenerative
 CC oligonucleotide primers: a first set which amplifies all PTK DNA
 CC segments (AA049743-44), and a second set which amplifies highly
 CC conserved sequences present in the catalytic domain of the c-kit
 CC subgroup of PTKs (AA049745-46). The PTK genes identified are described
 CC in AA049747-57 and AA041540-02.
 CC SAL-S1 is expressed in several megakaryocytic cell lines, but not
 CC in erythroid cell lines. The SAL-S1 expression prod. exhibited
 CC significant sequence homology with known protein tyrosine kinases
 CC of the FLT/FLK family. The partial and full-length SAL-S1 gene
 CC sequences are given in AA049747 and AA049753 respectively.
 XX
 SO Sequence 6827 BP; 1555 A; 1868 C; 1740 G; 1660 T; 4 other;
 Query Match 25.3%; Score 1040.2; DB 14; Length 6827;
 Best local Similarity 38.3%; Prod. No. 2,10-199;
 Matches 1051; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 2827 GCGGGCTTCGAAAGACCGAGCGCGAGCGCGGGCTTCTCCAGACCAAGACCTGAG 2768
 QY 3026 GACCTGGCTAGGCCCGCTGACCATGAGATCTGTCTGCTAGCTTCCAGCTGGCC 3085
 Db 2767 GACCTGGCTAGGCCCGCTGACCATGAGATCTGTCTGCTAGCTTCCAGCTGGCC 2708
 QY 3086 AGAGGATGACCTTCTGGCTTCCGAAAGCTCATCACAGACCTGGCTGCGGAGC 3145
 Db 2707 AGAGGATGAGCTTCTGGCTTCCGAAAGCTCATCACAGACCTGGCTGCGGAGC 2648
 QY 3146 ATTCTGCTGCGAAAGCGACGTGGTGAAGATCTGTGACTTGGCTTCCCGGACATC 3205
 Db 2647 ATTCTGCTGCGAAAGCGACGTGGTGAAGATCTGTGACTTGGCTTCCCGGACATC 2588
 QY 3206 TACAAAGACCTGACTAGCTCCGCAAGGCGATGCCCCGCTCCCTGTAAGTGAATGCC 3265
 Db 2587 TACAAAGACCTGACTAGCTCCGCAAGGCGATGCCCCGCTCCCTGTAAGTGAATGCC 2528
 QY 3286 CTTGAAAGCATCTTCGACAAAGGTGTACACACCGACAGTGAATGCTGCTTGGGGTG 3325
 Db 2527 CTTGAAAGCATCTTCGACAAAGGTGTACACACCGACAGTGAATGCTGCTTGGGGTG 2468
 QY 3326 CTTCTGGAAGATCTTCTCTGAGGGGCTCCCTGCTACCTGAGGCTGCAATCATGAG 3385
 Db 2467 CTTCTGGAAGATCTTCTCTGAGGGGCTCCCTGCTACCTGAGGCTGCAATCATGAG 2408
 QY 3386 GAGTCTCCGACGCGCTGAGAGACGCGACAAAGATAGAGGCCCGGAGCTGCTCCTCC 3445
 Db 2407 GAGTCTCCGACGCGCTGAGAGACGCGACAAAGATAGAGGCCCGGAGCTGCTCCTCC 2348
 QY 3446 GCCATAGCCCGCATATGCTGACCTGCTGCTGCGAGACCCCAAGCGAGCTGCATTC 3505
 Db 2347 GCCATAGCTGCTATGCTGACCTGCTGCTGCGAGACCCCAAGCGAGCTGCATTC 2288
 QY 3506 TCGAGCTGATGATGATCTCTGAGGACCTCTCCAGAGCGAGGCTCTGCAAGAGAAAGAG 3565
 Db 2287 TCGAGCTGATGATGATCTCTGAGGAGCTCTCCAGAGCGAGGCTCTGCAAGAGAAAGAG 2228
 QY 3566 GAGTCTGATGAGCCCGCGACGCTCTGAGAGCTTCAAGAGAGGAGCTTCTGAGAGTG 3625
 Db 2227 GAGTCTGATGAGCCCGCGACGCTCTGAGAGCTTCAAGAGAGGAGCTTCTGAGAGTG 2168
 QY 3626 TCCACCATGCGCCCTACATGACCTGCGCAGCTGAGAGACGCGCGCAAGCTGTGAG 3685
 Db 2167 TCCACCATGCGCCCTACATGACCTGCGCAGCTGAGAGACGCGCGCAAGCTGTGAG 2108
 QY 3686 CGCCAGAGCTGCGCGCGCGACGCTATTACAGCTGGGTCTCTTCCGGGTGCTGCGCAGA 3745
 Db 2107 CGCCAGAGCTGCGCGCGCGACGCTATTACAGCTGGGTCTCTTCCGGGTGCTGCGCAGA 2048
 QY 3746 GGGGCTGAGACCGCGTGTCTCTGAGATGAACATTTGAGAAATTCCTCATGACCCA 3805
 Db 2047 GGGGCTGAGACCGCGTGTCTCTGAGATGAACATTTGAGAAATTCCTCATGACCCA 1988
 QY 3806 ACGACCTAAGAGCTCTGTGACACCAAGACAGAGTGGATGCTGCTGCTGCGAG 3865
 Db 1987 ACGACCTAAGAGCTCTGTGACACCAAGACAGAGTGGATGCTGCTGCTGCGAG 1928
 QY 3866 GAGTTGAGCAATAGAGAGCGCATATGACAAAGAAAGCGGCTTCACT 3914
 Db 1927 GAGTTGAGCAATAGAGAGCGCATATGACAAAGAAAGCGGCTTCACT 1879
 RESULT 13
 AAT03101/c
 ID AAT03101 standard; DNA; 6827 BP.
 XX
 AC AAT03101;
 XX
 DT 14-FEB-1996 (first entry)
 XX
 DE Protein tyrosine kinase SAL-S1 gene.
 XX

Db 2085 TTCCAGAAAGCTCTCTGAGAGACCAAGGAGCTATGTTTCTCTCTCTCTCAAGTAAGAG 2145
 Qy 2597 AGGATGATGATGAGACTGCTGATGAGAGATGCTGTGTGAGAGGCTGAGAGCCCTCGG 2056
 Db 2146 ACCAGAGAAAGCATTGCTGTGTGAAACAGCTCAATCTCTAGAGCCATGCGACCCATG 2205
 Qy 2057 CTATCCAGCAATCTGAGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2116
 Db 2206 ATCCAGCAATCTGAG 2265
 Qy 2117 TGGTGGCCGAG 2176
 Db 2266 CAGCATCTGAG 2325
 Qy 2177 GAAAGTCTGAG 2236
 Db 2326 GAGAGATGAG 2385
 Qy 2237 GAG 2296
 Db 2386 AAG 2445
 Qy 2297 TCGGAG 2356
 Db 2446 GAG 2505
 Qy 2357 GTGAG 2416
 Db 2506 GTGAG 2565
 Qy 2417 ATGAG 2476
 Db 2566 GTTAAAG 2625
 Qy 2477 GAG 2536
 Db 2626 GATGAG 2685
 Qy 2537 TTGAG 2596
 Db 2686 TTGAG 2745
 Qy 2597 GTGAG 2656
 Db 2746 ATGAG 2805
 Qy 2657 ATGAG 2716
 Db 2806 ATGAG 2865
 Qy 2717 GTGAG 2776
 Db 2866 GTGAG 2925
 Qy 2777 GAG 2836
 Db 2926 GAG 2985
 Qy 2837 GAG 2896
 Db 2986 GAG 3045
 Qy 2897 TTGAG 2956
 Db 3046 AAG 3105
 Qy 2957 GTGAG 3016
 Db 3106 AAG 3165
 Qy 3017 GAG 3070

Db 3166 GAG 3225
 Qy 3071 AGCTTCCAG 3130
 Db 3226 AGCTTCCAG 3285
 Qy 3131 CTGAG 3190
 Db 3286 CTGAG 3345
 Qy 3191 CTGAG 3250
 Db 3346 TTGAG 3405
 Qy 3251 CTGAG 3310
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 Qy 3371 GTGAG 3430
 Db 3526 GTGAG 3585
 Qy 3431 GAGCTGGCAG 3490
 Db 3586 GAGCTGGCAG 3645
 Qy 3491 GCGAG 3550
 Db 3646 GAG 3705
 Qy 3551 CTGAG 3607
 Db 3706 GAG 3762

RESULT 15
 AAX77516
 ID AAX77516 standard; cDNA: 5404 BP.
 XX
 AC AAX77516;
 DT 05-APR-1999 (first entry)
 XX
 DE Murine f.k-1 cDNA.
 XX
 KW Murine f.k-2; f.k-1; cell isolation; fetal liver kinase; receptor;
 KW monoclonal; polyclonal; antibody; tyrosine kinase; ds.
 OS Mus sp.
 XX
 FT key location/Qualifiers
 FT CDS 208..431
 FT /-tag- a
 FT /product- "f.k-1"
 XX
 PN US912133-A.
 XX
 PD 15-JUN-1999.
 XX
 PE 10-FEB-1998; 9805-0021324.
 XX
 PR 19-NOV-1992; 9205-0977451.
 PR 02-APR-1991; 9105-0679666.
 PR 28-JUN-1991; 9105-0728913.
 PR 15-NOV-1991; 9105-0793065.
 PR 24-DEC-1991; 9105-0813593.
 PR 26-JUN-1992; 9205-0906397.
 PR 12-NOV-1992; 9205-0975049.
 PR 30-APR-1993; 9305-0055269.

QY	2177	GAAGAAGCTGAGATCGATCTGCGGAGATCGAAGCGAAGGCTGAGATATCCAGCGGTGGCC	2230
DB	2126	SAGAGTTCAGATATTGTAATGATGATGAGAGATGGGAATCGGAATCTGTACTATCCGAGAGCTGAG	2385
QY	2237	GAGGAGATGCGGAGAGGATATCTGTGAGATGTGTGTGCAAGCGAGGTGTGTCACTCC	2296
DB	2286	AAGGAGGATAGAGGAGCTTTTAACTGTGCAAGGCTTCCATTTCTTGGCTGTGTAAAGGG	2445
QY	2297	TCCGCGTACCGCTGAGCTGTGGAAGGCTGTGAGGATTAACCGGAGCTGGAGATGTGTATCTT	2356
DB	2446	GAGAGGCTTCTTCAATATGAAAGGTGGCCGAGAAAGAAATACATGTGAAGTATTATCTTC	2505
QY	2357	GTCGGTACCGGAGTATGAGTGTGTCTTTCTTGTGGGTGTGTGTCTGTCTATCTTGTAA	2416
DB	2506	GTCGGGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2565
QY	2417	ATGAGGAGAGCGGAGCGCCAGCGGAGATATCAAGATAGGAGTCTGTTCATATATGACGCC	2476
DB	2566	GTTTAAGCGCGCCCAATGAAAGGAGATGAAAGAGAGGAGATGATGATGATGATGATGATG	2625
QY	2477	GGCGAGGTGCTGTGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATG	2536
DB	2626	GATGAATTTGCCCTGTGATGAGAGAGTGTGTGAAGGCTGTGTGTATATATGAGCAAGTGG	2685
QY	2537	TTCCGCGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG	2596
DB	2686	TTCCGCGAGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG	2745
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DB	2746	ATTGAGATGAGAGCTTTTGTGTATGATGATGATGATGATGATGATGATGATGATGATG	2805
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DB	2806	ATGCGAAG	2865
QY	2717	GTATGATGATGAG	2776
DB	2866	GTATGATGATGAG	2925
QY	2777	GAG	2836
DB	2926	GAG	2985
QY	2837	GAG	2896
DB	2986	GAG	3045
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DB	3046	TTCGAG	3105
QY	2957	GTCGATGTCGCGGAGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3016
DB	3106	GTCGATGTCGCGGAGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3165
QY	3017	GAG	3079
DB	3166	GAG	3225
QY	3071	ACCTTTCAG	3130
DB	3226	ACCTTTCAG	3285
QY	3131	GTCGATGTCGCGGAGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3190
DB	3286	GTCGATGTCGCGGAGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3345
QY	3191	GTCGATGTCGCGGAGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3250
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Job time : 874 secs

Search completed: May 1, 2003, 06:42:44
Job time : 874 secs

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LOCUS AR016568 4195 bp DNA linear PAT 05 DEC 1998
DEFINITION Sequence 1 from patent US 5776755.
ACCESSION AR016568
VERSION AR016568.1 GI:3572845
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4195)
AUTHORS Allitalo, K., Aprelikova, O., Pajusola, K., Armstrong, E., Kornonen, J., and Kallajainen, A.
TITLE YU4, a receptor tyrosine kinase
JOURNAL Patent: US 5776755-A 1 07-Jul-1998;
FEATURES
location/qualifiers
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source
organism="Unknown"

BASE COUNT 985 a 1279 c 1305 g 722 t
ORIGIN

Query Match 95.2% Score 3912.4; DB 6; Length 4195;
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RESULT 6

DEFINITION H-sapiens mRNA for FLT4, class III receptor tyrosine kinase.
 ACCESSION X68203
 VERSION X68203.1 GI:31433
 KEYWORDS FLT4; tyrosine kinase receptor.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 4416)
 AUTHORS Aprelikova, O.
 JOURNAL Direct Submission
 Submitted (07-SEP-1992) C. Aprelikova, University of Helsinki, Cancer Biology Laboratory, Dept of Pathology, Haartmaninkatu 3, 00290 Helsinki, FINLAND
 REFERENCE 2 (bases 1 to 4416)
 AUTHORS Aprelikova, O., Pajusola, K., Partanen, J., Armstrong, E., Allitalo, R., Bailey, S. K., McMahon, J., Masumoto, J., Huebner, K., and Allitalo, K.
 TITLE FLT4, a novel class III receptor tyrosine kinase in chromosome 5q31-qter.
 JOURNAL Cancer Res. 52 (3), 746-748 (1992)
 MEDLINE 9219639
 COMMENT 1310071
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SOURCE	UNKNOWN.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 4425)		
AUTHORS	Bennett,B.D., Goeddel,D. and Matthews,W.		
TITLE	Protein Tyrosine Kinase against antibodies		
JOURNAL	Patent: US 5635177-A 31 03-JUN-1997;		
FEATURS	Location/Qualifiers		
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DB 1683 CCGCGAGCGCTTCACCATGCAATCCAGACATCCGAGAGCTACTAGAGGGCGACCGGGT 1742
QY 1741 GCTGCTGAGCTTCCAAAGCTGAGCTAGCAAGTACGAGCAATCTGGCGTGTACCGGCTCAA 1800
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[illegible]

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DEFINITION	AF402785		
ACCESSION	AF402785.1	GI:16033526	
KEYWORDS			
ORGANISM	Rattus norvegicus		
SOURCE	Rattus norvegicus		
REFERENCE	1 (bases 1 to 4360)		
AUTHORS	Krishnan, J. and Sleeman, J. P.		
TITLE	Characterization of a novel alternatively spliced form of VEGFR-3		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 4360)		
AUTHORS	Krishnan, J. and Sleeman, J. P.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik, Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021, Germany		
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 GY 3980 GAGGCT 4039
 Db 3961 GAGGCT 4020
 GY 4040 TCGAGAGCTCTGAGAGCATAGAGAGCGCATACAGAGAAAGCGCTCTCTCTCTCTCT 4099
 Db 4021 TCGAGAGCTCTGAGAGCATAGAGAGCGCATACAGAGAAAGCGCTCTCTCTCTCTCT 4080
 GY 4100 AAGGCT 4111
 Db 4081 AAGGCT 4092
 RESULT 14
 AF402786 4254 bp mRNA MOD 11-OCT-2001
 LOCUS AF402786
 DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3kt (Vegfr3) mRNA,
 complete cds, alternatively spliced.
 ACCESSION AF402786
 VERSION AF402786.1 GI:16033529
 KEYWORDS
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 4254)
 AUTHORS Krishnan,J. and Sleeman,J.P.
 TITLE Characterization of a novel alternatively spliced form of VEGFR-3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4254)

[illegible]

QY	2600	GAAGCCCTCGCTTTGGGATCTGCACAAAGGAGACACTGTGCACACCTGGGCGCGGAAATG	2659
DB	2591	GAAGCCTCAGCCTTTGGCATTAATAAAGGAGACACTGTGATACCGTGGCGGTGAAGATG	2640
QY	2650	CTGAAAGAGGGGCCACGGGCGAGCAGCACACCGCGCTGATGTGAGACTCAAGATCTCT	2719
DB	2641	CTGAAAGAGGGCGCTACAGCCCTTAATGTGGTAACTCCTCTGAGGGCGGTACACCAAGCTCCAT	2760
QY	2780	GGGCCCCCTCATGGTATGTTGAGATCTGCAAGTTCAGGCAACCTCTGCACCTTCGCGGC	2839
DB	2761	GGGCGCTCTCATGGTATGTTGAGATCTTTCGAAATACGGCAACCTCTGCACCTTTCTGGCT	2820
QY	2840	GCCAAAGCGGAGCGCTTACGCCCTGCGGGGAAAGTCTCCGAGCAGCGCGGACGCTTC	2899
DB	2821	GTCAAAGCGGAGACCTTGCACCCCTACGAGAGAGTCTCCCGAGCAAGCGTACCGGCTTC	2880
QY	2900	CGCGCCATGGTGGACTCTGACAGGTGAGATGAGAGCGGCGGGGAGACACCAACAGGGTC	2959
DB	2881	CGCGCGATGGTGAAGAGCGGTGAAGAGTGTGATAGAGAGACCTTGAAGACCGCGCAAGCC	2940
QY	2960	CTCTTGCCCGGCTTCTCGCAAGCCGAGACCGAGCGGCGGCTCCACAGCCAAAGAA	3019
DB	2941	CTGTTTACAAAGTCTCTCATATGGCCAAAGAAAGTGCACGGGCGAGGCCCATTTGTCACAGAA	3000
QY	3020	GCTGAGGACCTGTGGCTGACGCGCGCTGACCATGAGAAATCTGTGCTGATACAGCTTCAG	3079
DB	3001	GCTGAGACCTGTGGTGTGACCGCGCTGACCATGAGAGACCTGTGCTGATACAGCTTCCAA	3060
QY	3080	GTCGCGCAGAGGGATGAGTTCCTGCGCTCCCGCAAAAGTGCATCCACAGACACCTGGTGCCT	3139
DB	3061	GTCGCGCGGGGAATGAGTTCCTGCGCTCCCGCAAGTGCATCCACAGACACCTGGTGCCT	3120
QY	3140	CGGAAATCTCTGCTGTCGGAAGGCAACGTGGTGAAGATCTGTACTTTGGCCTTGGCCGC	3199
DB	3121	CGGAAATCTTACTGTACGAAAGTGACATGAGAAATCTGTGACTTTGGCCTTCCTCGGG	3180
QY	3200	GACATCTACAAAGACCCGTGACTAGCTGCGCCGAGAGGACAGTGGCGGCTCGCCCTGAAAGTGG	3259
DB	3181	GACATCTACAAAGACCCGTGACTAGCTGCGGAAAGGCGACGCGCCGACT-----	3227
QY	3260	ATGGCCCCCTGAAAGCATTTCTGACAAAGTGTCACCCACAGAGTGAAGCTGTGTCCTTT	3319
DB	3228	-----	3227
QY	3320	GGGCGTCTCTGCGGAGATCTCTCTGCGGGGCGCTCCCGTACCTGGGGGTGAGATC	3379
DB	3328	-----GGCTTCTCATACCTTGGGGTATACGATC	3254
QY	3380	AATGAGGAGTCTTGCACCGGCTGAGACAGCGCACAAAGATGAGGGGCCCGGAGCTGGCC	3439
DB	3255	AATGAGGAGTCTTGCACCGGCTGAGAGCGGCACAAACGAAATGAGGGGCCCAAAATCTGGCC	3314
QY	3440	ACTCCCGCATACGCGCATATGCTGAGACTCTGTGCGGAGAACCCCAAGGCGAGACTCT	3499
DB	3315	ACTCTCGCATACGCGCATATGCTGAGAGTCTGTGAGACCCCTTAAACCGAGGCTCT	3374
QY	3500	GCAATCTCGGACCTGGTGGAGATCTCTGGGGAGCTGTCTCCAGGGCAGGGGCTCTGCAMAGC	3559
DB	3375	GCATCTCTGAGCCTAGTGGAGATCTGGGGGAGCTGTCTTCAAGGTGGAGGCTGGAGAG	3434
QY	3560	GAAAGAGAGTGTGATATGGCCCCCGGAGCTCTCAGAGACTTGAAGAAGGCGACGTTCTCG	3619
DB	3435	GAGGAGAGAGATGTATGACCCCTGCACAGCTTTCAGAGACTTACAGGAGAGATGGCTTCTATG	3494
QY	3620	CAGGTTCCACCATGGCCTTCAACATGCTCCAGAGTGAAGTGAAGACACCGCGCAAGC	3679
DB	3495	CAGGATCCACCAAGCCTCTATATATCAAGAGGCTGAAGAGTTCAGAGACAGTCCACCCAGC	3554
QY	3680	CTGACAGCGCACGCTTGGCGCGTAAGTAATTACAACTGGGTCTCTTCTCCCGGAGTGCCTC	3739

Db 2677 GCTTTTGGGATCATTAATAACACAGCTGTAGACCTTACAGCTAAATTCCTGAACAG 2736
 2699 GGGGACAGGCTCAGCGAGTACCGCGGCTGATTCGGAGSTCAAGATTCCTATTCATTC 2728
 Db 2737 GAGGCTGCTGAAGTGAACGAAAGGACGATGTACAGCTGAAATTCCTCATTCACAT 2796
 2729 GGTAAACCACTGACGTTGGTCAACCTCCCTCGGGGCTGGACCAAGCCGAGGCGCCCTC 2788
 Db 2797 GGAAGCAGACTGAACGCTGGTGAATTTGCTGGTGTCTGTACCAACCCCAATGCTCACTC 2856
 2789 ATGCTGATCTGAGATCTGCAAGTACGCAACCTCTCCACTTCCTCCGCCCAAGCGG 2848
 Db 2857 ATGCTTATCTGCTGATGTGCAAGTATGGCAACCTCTCCAAATTAAGCTGGAGCAACGGA 2916
 2849 GAGGCTCTCAGCCCTTCGCGAGAGAACTCTCCGAGAGCGCGGAGGCTTCCGGCCATG 2908
 Db 2917 GAGGATTCATCCCTACAGGAGAACTCACAGGCTTGGCTTTCAGCTCCAGTCAATT 2976
 2909 GTGGAGCTGGCAAGCTGGA---TCGGAGGCGGCGGGGAGCAGGACAGAGGCTCTCTC 2965
 Db 2977 GTGGAGGAGTGAAGAGCGAGCAAGAGAGTGGCTGTGGACTGTGACAGAGTATCTTC 3036
 2966 GGCCTGCTTCTGCAAGAGTGAAGCGGAGCAAGCGGCGGCTCTCCAGACCAAGAGCTGAG 3025
 Db 3037 AACGCTTCTGATGAGCAAGAGCGAGAGCTACAG-----CCAAATCCAGGAAGTGGAT 3090
 3026 GAGCTGTGAGCTGAGCGCGGCTGACCTGACATGTAATCTCTGTCTGACAGCTTCAGAGTGGC 3085
 Db 3091 GAGCTGTGAGCAAGTCTGCTGAGCAAGTGAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTG 3150
 3086 AAGGAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3145
 Db 3151 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3210
 3146 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3205
 Db 3211 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3270
 3206 TACGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3265
 Db 3271 TACGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3330
 3266 CCTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3325
 Db 3331 CCAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3390
 3326 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3385
 Db 3391 CCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3450
 3386 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3445
 Db 3451 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3510
 3446 GGCATACCCGCACTCATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3505
 Db 3511 GAAATTTACCGTATATATGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3570
 3506 TCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3565
 Db 3571 TCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3627
 3566 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3625
 Db 3628 AAGCATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3687
 3626 TCGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3685
 Db 3688 CTTCTG 3741
 3686 CCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3745

Db 3742 TGTACAGCTTAGCAGCAAGATATTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3801
 3746 GGGGCTGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3805
 Db 3802 GGAATTCAGATCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3861
 3806 ACGACCTCAAAAGCTCTGTGAGCAACGAGCAGAGTGGATGGTGGCTGGCTGGAG 3865
 Db 3862 ACATATGTACAAAGGCAACCGGCAATTCAGCAGAGCTGGATGTTTGGCATCTGAG 3921
 3866 GAGTTGAGCAGATAGAGAGCAGCATAAGCAAGAAACCGGCTTCAGCTGTAAAGAGCT 3925
 Db 3922 GAATTTGAGAGATAGAAAACGACAGCAAAAGAGTGGATTCAAGCAGCAAAAGGCGC 3981
 3926 GGCAGAAATGTGCTGTGACAGAGGCAACCTGACTCTCCAAAGGAGCGCGGCTGCT 3985
 Db 3982 AACCACTGGGAGGCTGTGAGCAGAACGTCAGCTGCGGAGCAGATGTGCGGCTCA 4041
 3986 GAGCGGGGGGCGCAGAGGCGCAGTGTGTTTAAACAGCGCAATAGGGAGCTGTGGAG 4045
 Db 4042 TACGATCCCGAGTGGAGGCGCAGCTTTTACAAACAGTGAATAGGGAGCTGTGAGAA 4101
 4046 CCAAGCAGAGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4077
 Db 4102 CACTCTGAGAGCCGAGCTTCAACCCACCGCGC 4133

Search completed: May 1, 2003, 09:32:27
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